Input file Fbh32142FL.seq; Output File 32142.trans
Sequence length 2660

```
                                                                  M   A   A   T      4
CCTTTNTNRCCACGCGTCCGAGAGCGCCCCGCAGTCTTCGCGGAAAGCGTTCGGGGTAGGCG ATG GCT GCG ACG     12

 R   A   G   P   R   A   R   E   I   F   T   S   L   E   Y   G   P   V   P   E     24
CGT GCA GGG CCC CGC GCC CGC GAG ATC TTC ACC TCG CTG GAG TAC GGA CCG GTG CCG GAG     72

 S   H   A   C   A   L   A   W   L   D   T   Q   D   R   C   L   G   H   Y   V     44
AGC CAC GCA TGC GCA CTG GCC TGG CTG GAC ACC CAG GAC CGG TGC TTG GGC CAC TAT GTG    132

 N   G   K   W   L   K   P   E   H   R   N   S   V   P   C   Q   D   P   I   T     64
AAT GGG AAG TGG TTA AAG CCT GAA CAC AGA AAT TCA GTG CCT TGC CAG GAT CCC ATC ACA    192

 G   E   N   L   A   S   C   L   Q   A   Q   A   E   D   V   A   A   A   V   E     84
GGA GAG AAC TTG GCC AGT TGC CTG CAG GCA CAG GCC GAG GAT GTG GCT GCA GCC GTG GAG    252

 A   A   R   M   A   F   K   G   W   S   A   H   P   G   V   V   R   A   Q   H    104
GCA GCC AGG ATG GCA TTT AAG GGC TGG AGT GCG CAC CCC GGC GTC GTC CGG GCC CAG CAC    312

 L   T   R   L   A   E   V   I   Q   K   H   Q   R   L   L   W   T   L   E   S    124
CTG ACC AGG CTG GCC GAG GTG ATC CAG AAG CAC CAG CGG CTG CTG TGG ACC CTG GAA TCC    372

 L   V   T   G   R   A   V   R   E   V   R   D   G   D   V   Q   L   A   Q   Q    144
CTG GTG ACT GGG CGG GCT GTT CGA GAG GTT CGA GAC GGG GAC GTC CAG CTG GCC CAG CAG    432

 L   L   H   Y   H   A   I   Q   A   S   T   Q   E   E   A   L   A   G   W   E    164
CTG CTC CAC TAC CAT GCA ATC CAG GCA TCC ACC CAG GAG GAG GCA CTG GCA GGC TGG GAG    492

 P   M   G   V   I   G   L   I   L   P   P   T   F   S   F   L   E   M   M   W    184
CCC ATG GGA GTA ATT GGC CTC ATC CTG CCA CCC ACA TTC TCC TTC CTT GAG ATG ATG TGG    552

 R   I   C   P   A   L   A   V   G   C   T   V   V   A   L   V   P   P   A   S    204
AGG ATT TGC CCT GCC CTG GCT GTG GGC TGC ACC GTG GTG GCC CTC GTG CCC CCG GCC TCC    612

 P   A   P   L   L   L   A   Q   L   A   G   E   L   G   P   F   P   G   I   L    224
CCG GCG CCC CTC CTC CTG GCC CAG CTG GCG GGG GAG CTG GGC CCC TTC CCG GGA ATC CTG    672

 N   V   V   S   G   P   A   S   L   V   P   I   L   A   S   Q   P   G   I   R    244
AAT GTC GTC AGT GGC CCT GCG TCC CTG GTG CCC ATC CTG GCC TCC CAG CCT GGA ATC CGG    732

 K   V   A   F   C   G   A   P   E   E   G   R   A   L   R   R   S   L   A   G    264
AAG GTG GCC TTC TGC GGA GCC CCG GAG GAA GGG CGT GCC CTT CGA CGG AGC CTG GCG GGA    792

 E   C   A   E   L   G   L   A   L   G   T   E   S   L   L   L   L   T   D   T    284
GAG TGT GCG GAG CTG GGC CTG GCG CTG GGG ACG GAG TCG CTG CTG CTG CTG ACG GAC ACG    852
```

Fig. 1A

```
A  D  V  D  S  A  V  E  G  V  V  D  A  A  W  S  D  R  G  P   304
GCG GAC GTA GAC TCG GCC GTG GAG GGT GTC GTG GAC GCC GCC TGG TCC GAC CGC GGC CCG   912

G  G  L  R  L  L  I  Q  E  S  V  W  D  E  A  M  R  R  L  Q   324
GGT GGC CTC AGG CTC CTC ATC CAG GAG TCT GTG TGG GAT GAA GCC ATG AGA CGG CTG CAG   972

E  R  M  G  R  L  R  S  G  R  G  L  D  G  A  V  D  M  G  A   344
GAG CGG ATG GGG CGG CTT CGG AGT GGC CGA GGG CTG GAT GGG GCC GTG GAC ATG GGG GCC  1032

R  G  A  A  A  C  D  L  V  Q  R  F  V  R  E  A  Q  S  Q  G   364
CGG GGG GCT GCC GCA TGT GAC CTG GTC CAG CGC TTT GTG CGT GAG GCC CAG AGC CAG GGT  1092

A  Q  V  F  Q  A  G  D  V  P  S  E  R  P  F  Y  P  P  T  L   384
GCA CAG GTG TTC CAG GCT GGT GAT GTG CCT TCG GAA CGC CCA TTC TAT CCC CCA ACC TTG  1152

V  S  N  L  P  P  A  S  P  C  A  Q  V  E  V  P  W  P  V  V   404
GTC TCC AAC CTG CCC CCA GCC TCC CCA TGT GCC CAG GTG GAG GTG CCG TGG CCT GTG GTC  1212

V  A  S  P  F  R  T  A  K  E  A  L  L  V  A  N  G  T  P  R   424
GTG GCC TCC CCC TTC CGC ACA GCC AAG GAG GCA CTG TTG GTG GCC AAC GGG ACG CCC CGC  1272

G  G  S  A  S  V  W  S  E  R  L  G  Q  A  L  E  L  G  Y  G   444
GGG GGC AGC GCC AGT GTG TGG AGC GAG AGG CTG GGG CAG GCG CTG GAG CTG GGC TAT GGG  1332

L  Q  V  G  T  V  W  I  N  A  H  G  L  R  D  P  S  V  P  T   464
CTC CAG GTG GGC ACT GTC TGG ATC AAC GCC CAC GGC CTC AGA GAC CCT TCG GTG CCC ACA  1392

G  G  C  K  E  S  G  C  S  W  H  G  G  P  D  G  L  Y  E  Y   484
GGC GGC TGC AAG GAG AGT GGG TGT TCC TGG CAC GGG GGC CCA GAC GGG CTG TAT GAG TAT  1452

L  R  P  S  G  T  P  A  R  L  S  C  L  S  K  N  L  N  Y  D   504
CTG CGG CCC TCA GGG ACC CCT GCC CGG CTG TCC TGC CTC TCC AAG AAC CTG AAC TAT GAC  1512

T  F  G  L  A  V  P  S  T  L  P  A  G  P  E  I  G  P  S  P   524
ACC TTT GGC CTC GCT GTG CCC TCA ACC CTG CCG GCT GGG CCT GAA ATA GGG CCC AGC CCA  1572

A  P  P  Y  G  L  F  V  G  G  R  F  Q  A  P  G  A  R  S  S   544
GCA CCC CCC TAT GGG CTC TTC GTT GGG GGC CGT TTC CAG GCT CCT GGG GCC CGA AGC TCC  1632

R  P  I  R  D  S  S  G  N  L  H  G  Y  V  A  E  G  G  A  K   564
AGG CCC ATC CGG GAT TCG TCT GGC AAT CTC CAT GGC TAC GTG GCT GAG GGT GGA GCC AAG  1692

D  I  R  G  A  V  E  A  A  H  Q  A  F  P  G  W  A  G  Q  S   584
GAC ATC CGA GGT GCT GTG GAG GCC GCT CAC CAG GCT TTC CCT GGC TGG GCG GGC CAG TCC  1752

P  G  A  R  A  A  L  L  W  A  L  A  A  A  L  E  R  R  K  S   604
CCA GGA GCC CGG GCA GCC CTG CTG TGG GCC CTG GCG GCT GCA CTG GAG CGC CGG AAG TCT  1812
```

Fig. 1B

```
 T   L   A   S   R   L   E   R   Q   G   A   E   L   K   A   A   E   A   E   V    624
ACC CTG GCC TCA AGG CTG GAG AGG CAG GGA GCG GAG CTC AAG GCT GCG GAG GCG GAG GTG  1872

 E   L   S   A   R   R   L   R   A   W   G   A   R   V   Q   A   Q   G   H   T    644
GAG CTG AGC GCA AGA CGA CTT CGG GCG TGG GGG GCC CGG GTG CAG GCC CAA GGC CAC ACC  1932

 L   Q   V   A   G   L   R   G   P   V   L   R   L   R   E   P   L   G   V   L    664
CTG CAG GTA GCC GGG CTG AGA GGC CCT GTG CTG CGC CTG CGG GAG CCG CTG GGT GTG CTG  1992

 A   V   V   C   P   D   E   W   P   L   L   A   F   V   S   L   L   A   P   A    684
GCT GTG GTG TGT CCG GAC GAG TGG CCC CTG CTT GCC TTC GTG TCC CTG CTG GCT CCC GCC  2052

 L   A   Y   G   N   T   V   V   M   V   P   S   A   A   C   P   L   L   A   L    704
CTG GCC TAC GGC AAC ACT GTG GTC ATG GTG CCC AGT GCG GCC TGT CCT CTG CTG GCC CTG  2112

 E   V   C   Q   D   M   A   T   V   F   P   A   G   L   A   N   V   V   T   G    724
GAG GTC TGC CAG GAC ATG GCC ACC GTG TTC CCA GCA GGC CTG GCC AAC GTG GTG ACA GGA  2172

 D   R   D   H   L   T   R   C   L   A   L   H   Q   D   V   Q   A   M   W   Y    744
GAC CGG GAC CAT CTG ACC CGC TGC CTG GCC TTG CAC CAA GAC GTC CAG GCC ATG TGG TAT  2232

 F   G   S   A   Q   G   S   Q   F   V   E   W   A   S   A   G   N   L   K   P    764
TTC GGA TCA GCC CAG GGT TCC CAG TTT GTC GAG TGG GCC TCG GCA GGA AAC CTC AAA CCG  2292

 V   W   A   S   R   G   C   P   R   A   W   D   Q   E   A   E   G   A   G   P    784
GTG TGG GCG AGC AGG GGC TGC CCG CGG GCC TGG GAC CAG GAG GCC GAG GGG GCA GGC CCA  2352

 E   L   G   L   R   V   A   R   T   K   A   L   W   L   P   M   G   D   *        803
GAG CTG GGG CTG CGA GTG GCG CGG ACC AAG GCC CTG TGG CTG CCT ATG GGG GAC TGA      2409

TGCCTGAGCGCCACCTACTGCATTTTGGACACCTCACACCAAGGGGAGATGCACCCCACAGACACCTGGGACTTTCCCC

TTCTGGTTCCTGTGTCTCCCAATAAACTCTCTGACCAACCCTAAAAAAAAAAAAAAAAAAAAAAAAAARWARMAACTTC

TGGCAGATATGAGGCTTTTTTCTTTTTTTTT
```

Fig. 1C

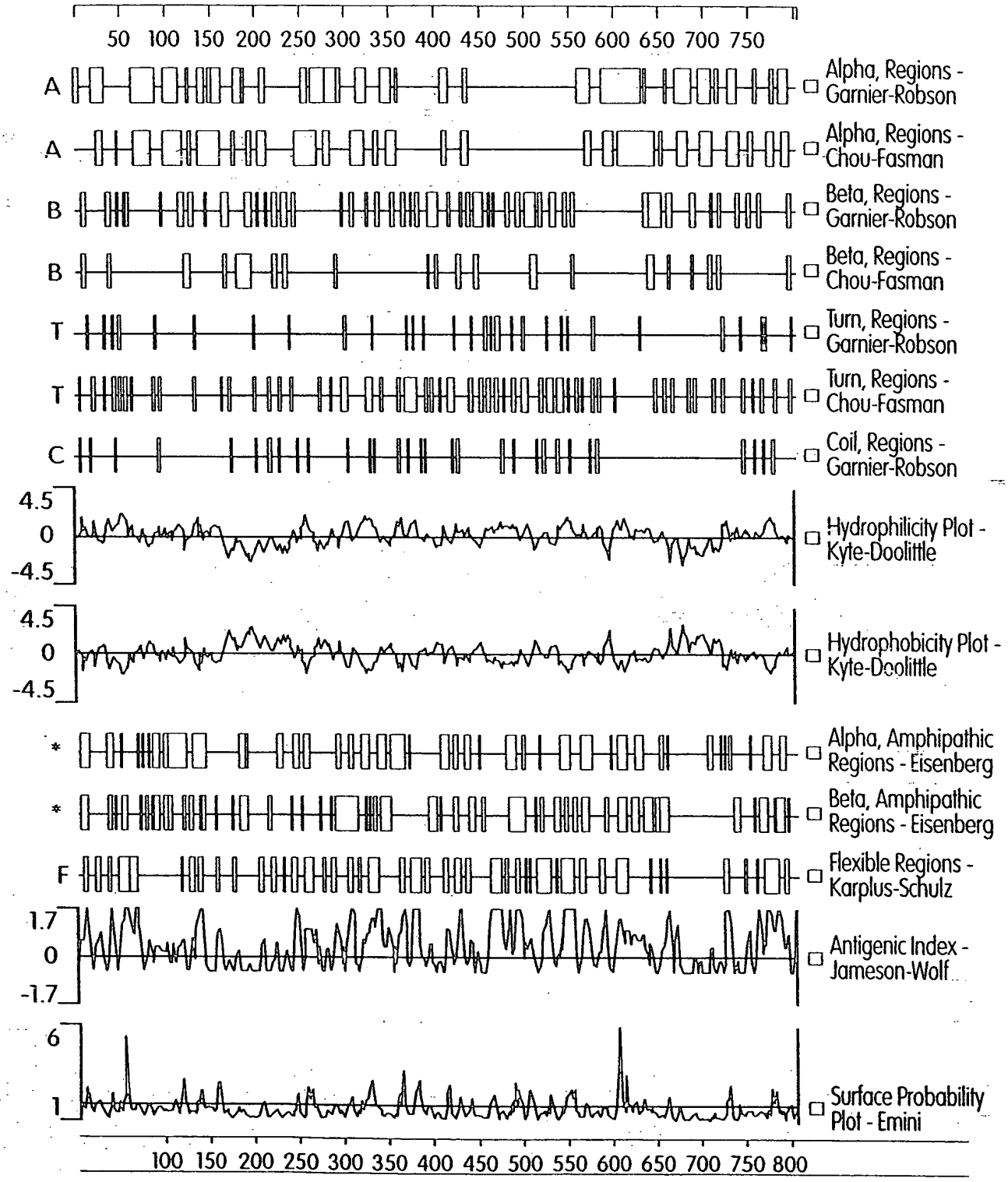

Fig. 2

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
159	175	ins-->out	0.1

>32142
MAATRAGPRAREIFTSLEYGPVPESHACALAWLDTQDRCLGHYVNGKWLKPEHRNSVPCQ
DPITGENLASCLQAQAEDVAAAVEAARMAFKGWSAHPGVVRAQHLTRLAEVIQKHQRLLW
TLESLVTGRAVREVRDGDVQLAQQLLHYHAIQASTQEEALAGWEPMGVIGLILPPTFSFL
EMMWRICPALAVGCTVVALVPPASPAPLLLLAQLAGELGPFPGILNVVSGPASLVPILASQ
PGIRKVAFCGAPEEGRALRRSLAGECAELGLALGTESLLLLTDTADVDSAVEGVVDAAWS
DRGPGGLRLLIQESVWDEAMRRLQERMGRLRSGRGLDGAVDMGARGAAACDLVQRFVREA
QSQGAQVFQAGDVPSERPFYPPTLVSNLPPASPCAQVEVPWPVVVASPFRTAKEALLVAN
GTPRGGSASVWSERLGQALELGYGLQVGTVWINAHGLRDPSVPTGGCKESGCSWHGGPDG
LYEYLRPSGTPARLSCLSKNLNYDTFGLAVPSTLPAGPEIGPSPAPPYGLFVGGRFQAPG
ARSSRPIRDSSGNLHGYVAEGGAKDIRGAVEAAHQAFPGWAGQSPGARAALLWALAAALE
RRKSTLASRLERQGAELKAAEAEVELSARRLRAWGARVQAQGHTLQVAGLRGPVLRLREP
LGVLAVVCPDEWPLLAFVSLLAPALAYGNTVVMVPSAACPLLALEVCQDMATVFPAGLAN
VVTGDRDHLTRCLALHQDVQAMWYFGSAQGSQFVEWASAGNLKPVWASRGCPRAWDQEAE
GAGPELGLRVARTKALWLPMGD

Fig. 3

Protein Family / Domain Matches, HMMer Version 2

```
Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)

Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:                 /prod/ddm/seqanal/PFAM/pfam5.0/Pfam
Sequence file:            /prod/ddm/wspace/orfanal/oa-script.9519.seq
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
 Query:  32142

Scores for sequence family classification (score includes all domains):
Model    Description                                        Score    E-value  N
-------- -----------                                        -----    ------- ---
aldedh   Aldehyde dehydrogenase family                       149.8    4.7e-41   1

Parsed for domains:
Model    Domain  seq-f,seq-t    hmm-f hmm-t      score  E-value
-------- ------- ----- ----- ..  ----- -----  []  -----  -------
aldedh     1/1      47   494 ..      1   492  []   149.8  4.7e-41

Alignments of top-scoring domains:
aldedh: domain 1 of 1, from 47 to 494: score 149.8, E = 4.7e-41
                  *->ewvdsasgktfevvNPankgevigrvpeataeDvdaAVkAAkeAfks
                     +w +++  + +++ +P + ge +++  +a+aeDv aAV AA+ Afk+
      32142    47    KWLWPEHRNSVPCQDPIT-GENLASCLQAQAEDVAAAVEAARMAFKG 92

                  GpwWakvpaseRariLrkladlieeredeLaaletlDlGKplaeAkgDte
                     W++ p   Ra+ L +la+ i+ ++ +L  le+l +G  ++e+  + +
      32142    93 ---WSAHPGVVRAQHLTRLAEVIQKHQRLLWTLESLVTGRAVREVRDG-D 138

                  vgraideiryyagwarklmgerrvipslatdgdeelnytrrePlGVvgvI
                  v+ a + ++y a +a+              t+   e ++  +eP GV+g I
      32142   139 VQLAQQLLHYHAIQAS-------------TQ---EEALAGWEPMGVIGLI 172

                  sPWNFPlllalwklapALAaGNTVVlKPSEqTPlt..alllaelieeaGa
                   P  F +l ++w ++pALA G+TVV   +   P+++  llla l  e G
      32142   172 LPPTFSFLEMMWRICPALAVGCTVV---ALVPPASpaPLLLAQLAGELG- 218

                  nnlPkGVvnvvpGfGaevGqaLlshpdidkisFTGSteVGklimeaAAak
                      +G +nvv G +a+ +  L+s+p+i+k++F G +e G+ + ++ A +
      32142   219 --PFPGILNVVSG-PASLVPILASQPGIRKVAFCGAPEEGRALRRSLAGE 265

                  nlkkVtLELGGKsPvIVfdDADLdkAverivfgaFgnaGQvCiApsRllv
                    +   L LG  s     d AD d Ave++v +a    G    ++ Rll+
      32142   266 -CAELGLALGTESLLLLTDTADVDSAVEGVVDAAWSDRG---PGGLRLLI 311

                  hesiydeFveklkervkklkliGdpldsdtniyGPlIseqqfdrvlsyIe
                  +es+ de + +l+er+ +l+  G +ld  + + G+   +++ d v +++
      32142   312 QESVWDEAMRRLQERMGRLR-SGRGLDGAVDM-GAR-GAAACDLVQRFVR 358

                  dgkeeGAkvlcGGerdeskeylggGyyvqPTiftdVtpdMkImkEEIFGP
                  +++++GA+v + G ++ +     +    ++ PT+++++ p +++++ E+  P
      32142   359 EAQSQGAQVFQAGDVPSE---RP---FYPPTLVSNLPPASPCAQVEVPWP 402

                  VlpiikfkdldEAIelaNdteYGLAayvFTkdilarafrvakaleaGiVw
                  V++   f++  EA+  aN t+ G +a+v+++  l  a     +l++G+Vw
      32142   403 VVVASPFRTAKEALLVANGTPRGGSASVWSER-LGQALELGYGLQVGTVW 451

                  vNDvcvhaaepqlPFGGvHqSSGiGrehgGkygleeYteiKtVtirl<-*
                  +N    ++ +p++P GG K+ SG + ++ G++gl eY++   +  rl
      32142   452 IN--AHGLRDPSVPTGGCKE-SGCSWHG-GPDGLYEYLRPSGTPARL    494
```

Fig. 4

ProDom Matches

ProdomId	Start	End	Description	Score
View Prodom 135 Boxer / Showing match / Go!	101	770	p99.2 (229) DHAL(10) DHAB(10) DHAM(7) // DEHYDROGENASE OXIDOREDUCTASE ALDEHYDE NAD PROTEIN CLASS SEMIALDEHYDE PRECURSOR TRANSIT PEPTIDE	280
ProdomId	Start	End	Description	Score

View Prodom 135 Boxer Showing match Go!

>135 p99.2 (229) DHAL(10) DHAB(10) DHAM(7) // DEHYDROGENASE OXIDOREDUCTASE ALDEHYDE NAD PROTEIN CLASS SEMIALDEHYDE PRECURSOR TRANSIT PEPTIDE
Length = 494

Score = 280 (103.6 bits), Expect = 7.8e-22, P = 7.8e-22
Identities = 87/289 (30%), Positives = 142/289 (49%)

```
Query:   216 ELGPFPGILNVVSG--PASLVPILASQPGIRKVAFCGAPEEGRALRRSXXXXXXXXXXXX 273
             E G  PG++NVV+G    A +   L S P I K++F G+ E G+A+ ++
Sbjct:   194 EAGLPPGVINVVTGFGGAEVGEALVSHPDIDKISFTGSTEVGKAIMKAAAEKNLKPVTLE 253

Query:   274 XXXXX--XXXXDTADVDSAVEGVVDAAWSDRGP---GGLRLLIQESVWDEAMRRLQERMG 328
                       D  D+D AVE VV  A+ + G        R+ +QES++DE + +L ER+
Sbjct:   254 LGGKNPVIVFEDADDLDKAVESVVFGAFFNSGQVCTAASRIFVQESIYDEFVEKLVERVK 313

Query:   329 RL-RSGRG--LDGAVDMGAR-GAAACDLVQRFVREAQSQGAQVFQAGD---VPSERPFY- 380
             +L + G    LD   DMG         + +Q ++ EA+++GA++   G+       E  ++
Sbjct:   314 KLLKVGEDDPLDPDTDMGPLINEEQYEKIQSYIEEAKAEGAKLVCGGERRKAGDEGGYFI 373

Query:   381 PPTLVSNLPPASPCAQVEVPWPVVVASPFRT-AKEALLVANGTPRGGSASVWSERLGQAL 439
              PT+++++        Q E+   PV+     F+     EA+ +AN T  G +A V++  + +A
Sbjct:   374 QPTILTDVTEDMRIMQEEIFGPVLPVIKFKDDLDEAIELANDTEYGLAAGVFTRDIERAQ 433

Query:   440 ELGYGLQVGTVWINA---HGLRDPSVPTGGCKESGCSWH-GGPDGLYEY 484
               +   L+ GTVW+N    H   +   P GG K+SG      GG  GL EY
Sbjct:   434 RVAERLEAGTVWVNDNIYHVSAEAQAPFGGYKQSGIGGREGGKYGLEEY 482

Score = 262 (97.3 bits), Expect = 8.2e-20, P = 8.2e-20
Identities = 86/301 (28%), Positives = 140/301 (46%)

Query:   101 RAQHLTRLAEVIQKHQRLLWTLESLVTGRAVREVRDGDVQLAQQLLHYHA---------- 150
             RA+ L +LA+++++++  L  LE+L TG+ + E +  +V  A   L Y+A
Sbjct:    61 RARILRKLADLLEENKDELAALETLETGKPLAEAKVAEVARAVDYLRYYAGMAEKLMGEE 120

Query:   151 -IQASTQEE----ALAGWEPMGVIGLILPPTFSFLEMMWRICPALAVGVTXX---XXXXX 202
              I  S  E      +    EP+GV+  I P  F  +  +W+I PALA G T
Sbjct:   121 TIPTSLSESPGSMSYTMREPLGVVAAITPWNFPLMMAVWKIAPALAAGNTVVLKPSEQTP 180

Query:   203 XXXXXXXXXXXXGELGPFPGILNVVSG--PASLVPILASQPGIRKVAFCGAPEEGRALRR 260
                         E G  PG++NVV+G    A +   L S P I K++F G+ E G+A+ +
Sbjct:   181 LTALLLAELIKEAEAGLPPGVINVVTGFGGAEVGEALVSHPDIDKISFTGSTEVGKAIMK 240

Query:   261 SXXXXXXXXXXXXXXXXX--XXXXDTADVDSAVEGVVDAAWSDPGP---GGLRLLIQESV 315
             +                    D  D+D AVE VV  A+ + G        R+ +QES+
Sbjct:   241 AAAEKNLKPVTLELGGKNPVIVFEDADDLDKAVESVVFGAFFNSGQVCTAASRIFVQESI 300

Query:   316 WDEAMRRLQERMGRL-RSGRG--LDGAVDMGAR-GAAACDLVQRFVREAQSQGAQVFQAG 371
             +DE + +L ER+ +L + G    LD   DMG         + +Q ++ EA+++GA++   G
Sbjct:   301 YDEFVEKLVERVKKLLKVGEDDPLDPDTDMGPLINEEQYEKIQSYIEEAKAEGAKLVCGG 360

Query:   372 D 372
             +
Sbjct:   361 E 361
```

Fig. 5A

```
 Score = 219 (82.2 bits), Expect = 4.9e-15, P = 4.9e-15
 Identities = 75/236 (31%), Positives = 105/236 (44%)

Query:   550 SSGNLHGYVAEGGAKDIRGAVEAAHQAFPG--WAGQSP-GXXXXXXXXXXXXXERRKSTL 606
             ++G +   V E   +D+  AVEAA +AF G  W   SP                E  K  L
Sbjct:    20 TNGEVIAQVPEATKEDVDKAVEAAREAFKGGEWGKTSPLSERARILRKLADLLEENKDEL 79

Query:   607 AS--RLERQGXXXXXXXXXXXXXXRRLRAW-GARVQAQGH-TLQVAGLRGP---VLRLRE 659
             A+   LE                    LR + G   +  G  T+  +    P       +RE
Sbjct:    80 AALETLETGKPLAEAKVAEVARAVDYLRYYAGMAEKLMGEETIPTSLSESPGSMSYTMRE 139

Query:   660 PLGVLAVVCPDEWPLLAFVSLLAPALATGNTVVMVPSAACPLLAL---EVCQDMATVFPA 716
             PLGV+A + P   +PL+   V  +APALA GNTVV+ PS    PL AL   E+ ++      P
Sbjct:   140 PLGVVAAITPWNFPLMMAVWKIAPALAAGNTVVLKPSEQTPLTALLLAELIKEAEAGLPP 199

Query:   717 GLANVVTG-DRDHLTRCLALHQDVQAMWYFGSAQ-GSQFVEWASAGNLKPVWASRG 770
             G+ NVVTG     +   L  D D+  + + GS + G    ++ A+  NLKPV    G
Sbjct:   200 GVINVVTGFGGAEVGEALVSHPDIDKISFTGSTEVGKAIMKAAAEKNLKPVTLELG 255
```

Fig. 5B

Input file Fbh21481FL.seq; Output File 21481.trans
Sequence length 1379

TTTGGCCCTCGAGGCCAAGAATTCGGCACGAGGAGCAAGTGGCCTTAACACATGGATTTTCTTCCAAAAATGCAGACCC

ATTTTAATTAAGTTTGTAATTAACCACTGGGGAGGGCAGGCCCCCTGGATTCGGTCTGCTTTCGGAGACACTGTGAGTA

ACTTCCTATTTGTTGAACATTTGGGGATTAGCACGCCCACTGGGTGTTCAGCTTGGAGGCTTGCACAGAGCTGAGCTCC

CTGCAGCCTTGGGCCTCCCCCTGCCCTGGGAGTCCTGATCAGCGTCTCTTTGCAAAGCCAATCCCCTTTTACTCCGTTG

```
                M  G  V  M  A  M  L  M  L  P  L  L  L  L  G  I    16
TCCCCCAGAACAAG ATG GGA GTC ATG GCC ATG CTG ATG CTC CCC CTG CTG CTG CTG GGA ATC   48

 S  G  L  L  F  I  Y  Q  E  V  S  R  L  W  S  K  S  A  V  Q    36
AGC GGC CTC CTC TTC ATT TAC CAA GAG GTG TCC AGG CTG TGG TCA AAG TCA GCT GTG CAG  108

 N  K  V  V  V  I  T  D  A  I  S  G  L  G  K  E  C  A  R  V    56
AAC AAA GTG GTG GTG ATC ACC GAT GCC ATC TCA GGA CTG GGC AAG GAG TGT GCT CGG GTG  168

 F  H  T  G  G  A  R  L  V  L  C  G  K  N  W  E  R  L  E  N    76
TTC CAC ACA GGT GGG GCA AGG CTG GTG CTG TGT GGA AAG AAC TGG GAG AGG CTA GAG AAC  228

 L  Y  D  A  L  I  S  V  A  D  P  S  K  T  F  T  P  K  L  V    96
CTA TAT GAT GCC TTG ATC AGC GTG GCT GAC CCC AGC AAG ACA TTC ACC CCA AAG CTG GTC  288

 L  L  D  L  S  D  I  S  C  V  P  D  V  A  K  E  V  L  D  C   116
CTG TTG GAC CTC TCA GAC ATC AGC TGT GTC CCA GAT GTG GCA AAA GAA GTC CTG GAT TGC  348

 Y  G  C  V  D  I  L  I  N  N  A  S  V  K  V  K  G  P  A  H   136
TAT GGC TGT GTG GAC ATC CTC ATC AAC AAT GCC AGT GTG AAG GTG AAG GGG CCT GCC CAT  408

 K  I  S  L  E  L  D  K  K  I  M  D  A  N  Y  F  G  P  I  T   156
AAG ATT TCT CTG GAG CTC GAC AAA AAG ATC ATG GAT GCC AAT TAC TTT GGC CCC ATC ACA  468

 L  T  K  A  L  L  P  N  M  I  S  R  R  T  G  Q  I  V  L  V   176
TTG ACG AAA GCC CTG CTT CCC AAC ATG ATC TCC CGG AGA ACA GGC CAA ATC GTG TTA GTG  528

 N  N  I  Q  G  K  F  G  I  P  F  R  T  T  Y  A  A  S  K  H   196
AAT AAT ATC CAA GGG AAG TTT GGA ATC CCG TTC CGT ACG ACT TAC GCT GCC TCC AAG CAC  588
```

Fig. 6A

```
 A   A   L   G   F   F   D   C   L   R   A   E   V   E   E   Y   D   V   V   I   216
GCA GCC CTG GGC TTC TTT GAC TGC CTC CGA GCC GAA GTG GAG GAA TAC GAT GTT GTC ATC  648

 S   T   V   S   P   T   F   I   R   S   Y   H   V   Y   P   E   Q   G   N   W   236
AGC ACC GTG AGC CCG ACT TTC ATC CGG TCG TAC CAC GTG TAT CCA GAG CAA GGA AAC TGG  708

 E   A   S   I   W   K   F   F   F   R   K   L   T   Y   G   V   H   P   V   E   256
GAA GCT TCC ATT TGG AAA TTC TTT TTC AGG AAG CTG ACC TAC GGC GTG CAC CCA GTA GAG  768

 V   A   E   E   V   M   R   T   V   R   R   K   K   Q   E   V   F   M   A   N   276
GTG GCG GAG GAG GTG ATG CGC ACC GTG CGG AGG AAG AAG CAA GAG GTG TTT ATG GCC AAC  828

 P   I   P   K   A   A   V   Y   V   R   T   F   F   P   E   F   F   F   A   V   296
CCC ATC CCC AAG GCC GCC GTG TAC GTC CGC ACC TTC TTC CCG GAG TTC TTT TTC GCC GTG  888

 V   A   C   G   V   K   E   K   L   N   V   P   E   E   G   *                   312
GTG GCC TGT GGG GTG AAG GAG AAG CTC AAT GTC CCG GAG GAG GGG TAA                   936

CTGCAGGAGGCCAAATGGGCCACCCCTTGGAAATAAAGGTTTTTCTGGCAAAAAAAAAAAAAAAAAAAAAANTTTGCGGC

CGCAAGCTTATTCCCTTTAGGGAGGGTTAATTTT
```

Fig. 6B

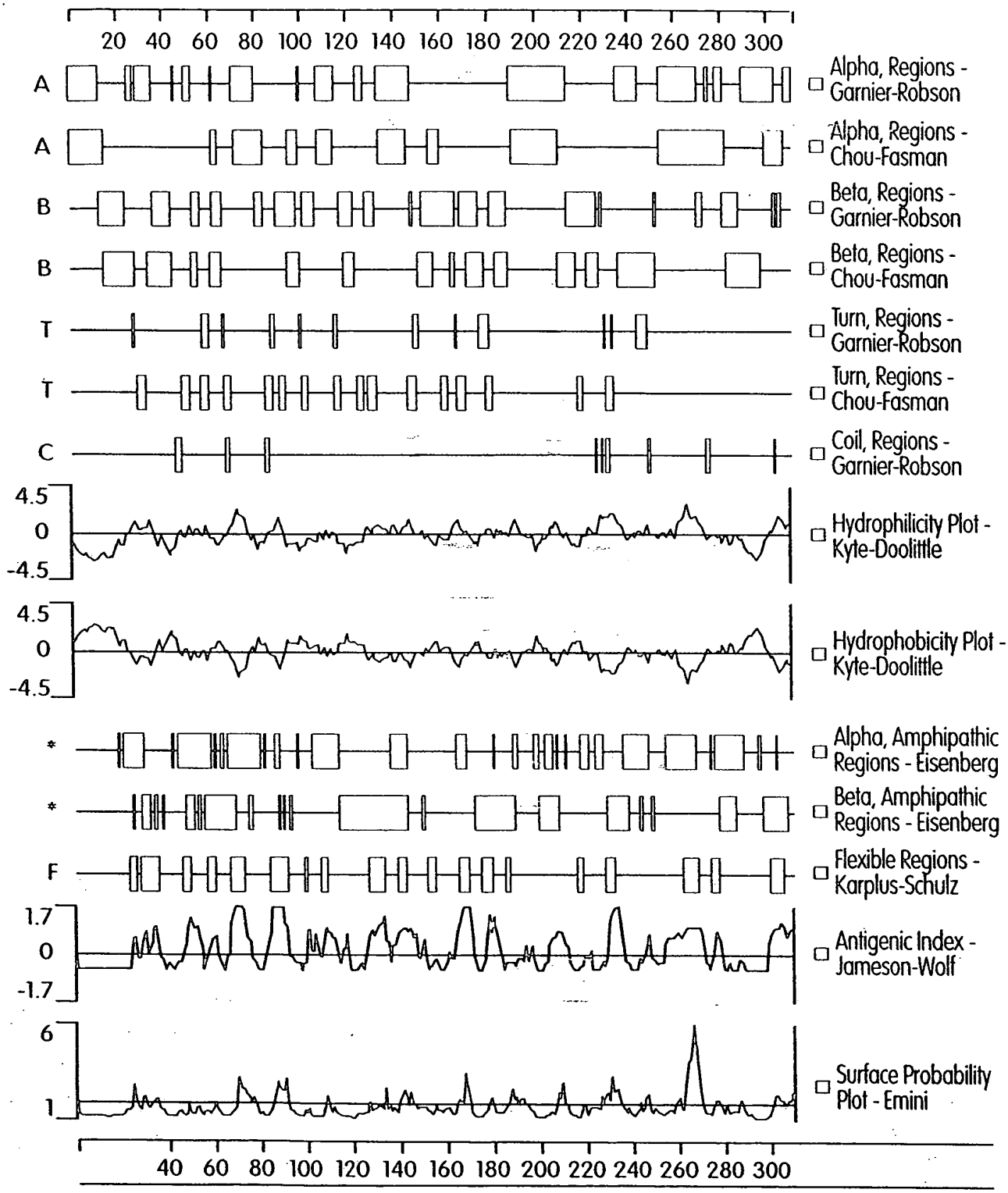

Fig. 7

Signal Peptide Predictions for 21481

Method	Predict	Score	Mat@
SignalP (eukaryote)	YES		19

Note: amino-terminal 70aa used for signal peptide prediction

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
7	23	ins-->out	4.5

>21481
MGVMAMLMLPLLLLGISGLLFIYQEVSRLWSKSAVQNKVVVITDAISGLGKECARVFHTG
GARLVLCGKNWERLENLYDALISVADPSKTFTPKLVLLDLSDISCVPDVAKEVLDCYGCV
DILINNASVKVKGPAHKISLELDKKIMDANYFGPITLTKALLPNMISRRTGQIVLVNNIQ
GKFGIPFRTTYAASKHAALGFFDCLRAEVEEYDVVISTVSPTFIRSYHVYPEQGNWEASI
WKFFFRKLTYGVHPVEVAEEVMRTVRRKKQEVFMANPIPKAAVYVRTFFPEFFFAVVACG
VKEKLNVPEEG

Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
265	283	ins-->out	0.2

>21481_mature
LLFIYQEVSRLWSKSAVQNKVVVITDAISGLGKECARVFHTGGARLVLCGKNWERLENLY
DALISVADPSKTFTPKLVLLDLSDISCVPDVAKEVLDCYGCVDILINNASVKVKGPAHKI
SLELDKKIMDANYFGPITLTKALLPNMISRRTGQIVLVNNIQGKFGIPFRTTYAASKHAA
LGFFDCLRAEVEEYDVVISTVSPTFIRSYHVYPEQGNWEASIWKFFFRKLTYGVHPVEVA
EEVMRTVRRKKQEVFMANPIPKAAVYVRTFFPEFFFAVVACGVKEKLNVPEEG

Fig. 8

Protein Family / Domain Matches, HMMer Version 2

```
Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:                 /prod/ddm/seqanal/PFAM/pfam5.0/Pfam
Sequence file:            /prod/ddm/wspace/orfanal/oa-script.9650.seq
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
 Query:  21481

Scores for sequence family classification (score includes all domains):
Model     Description                                        Score    E-value  N
--------  -----------                                        -----    -------  ---
adh_short  short chain dehydrogenase                          120.0    4.5e-32  1
A2M        Alpha-2-macroglobulin family                         0.5        7.1  1

Parsed for domains:
Model     Domain  seq-f seq-t    hmm-f hmm-t       score  E-value
--------  ------- ----- -----    ----- -----       -----  -------
adh_short   1/1      38   227 ..     1   203 []   120.0  4.5e-32
A2M         1/1     278   291 ..     1    14 [.     0.5      7.1

Alignments of top-scoring domains:
adh_short: domain 1 of 1, from 38 to 227: score 120.0, E = 4.5e-32
                   *->KvaLvTGassGIGlaiAkrLakeGakVvvadrneeklekGavakelk
                      Kv+++T a sG+G+++A+ +++ Ga++v+++ n e+le+    ++l
         21481    38    KVVVITDAISGLGKECARVFHTGGARLVLCGKNWERLEN--LYDALI 82

                   elGgnd..kdralaiqlDvtdeesv.aaveqaverlGrlDvLVNNAGgii
                      +++++      + lD++d + v+++++++++ +G +D+L+NNA   +
         21481    83 SV-ADPskTFTPKLVLLDLSDISCVpDVAKEVLDCYGCVDILINNAS--V 129

                   llrpgpfaelsrtmeedwdrvidvNltgvfllltravlplmamkkrggGrI
                       gp++++s   +e+ ++++d N++g++ lt+a+lp   m+ r+ G I
         21481   130 -KVKGPAHKIS---LELDKKIMDANYFGPITLTKALLP--NMISRRTGQI 173

                   vNiSSvaGrkegglvgvpggsaYsASKaAvigltrsLAlElaphgIrVna
                   v +  + G     + g p+++ Y+ASK+A  g+ ++L+ E+ ++ + ++
         21481   174 VLVNNIQG-----KFGIPFRTTYAASKHAALGFFDCLRAEVEEYDVVIST 218

                   VAPGgvdTd<-*
                   v+P +++
         21481   219 VSPTFIRSY    227

A2M: domain 1 of 1, from 278 to 291: score 0.5, E = 7.1
                   *->ideddtiRSyFPE<-*
                      i+   + +R++FPE
         21481   278    IPKAAVYVRTFFPE    291
```

Fig. 9

ProDom Matches

ProdomId	Start	End	Description	Score
View Prodom 11 Boxer / Showing match / Go!	99	219	p99.2 (1078) ADH(34) GALE(20) FABG(13)// OXIDOREDUCTASE PROTEIN DEHYDROGENASE NAD REDUCTASE NADP BIOSYNTHESIS SYNTHASE ALCOHOL PUTATIVE	113
ProdomId	Start	End	Description	Score

View Prodom 11 [Boxer] [Showing match] [Go!]

```
>11 p99.2 (1078) ADH(34) GALE(20) FABG(13)  // OXIDOREDUCTASE PROTEIN
    DEHYDROGENASE NAD REDUCTASE NADP BIOSYNTHESIS SYNTHASE ALCOHOL PUTATIVE
    Length = 269

 Score = 113 (44.8 bits), Expect = 0.00016, P = 0.00016
 Identities = 41/138 (29%), Positives = 63/138 (45%)

Query:    99 DLSDIS-CVPDVAKEVLDCYGCVDILINNASVKV-KGPAHKISLELD-----KKIMDANY 151
             D+ D+   V  V +E    +G +D+L+NNA V   K  A  ++ E       +++++ N
Sbjct:    87 DVEDVEKLVETVVEEFSGIHGKIDVLVNNAGVMAPKAVAESMTEETSDDEEWEEVIEVNV 146

Query:   152 FGPITLTKALLPNMIS--------RRTGQIVLVNNIQGK-FGIP-FRTTYAASKHAALGF 201
              G   LT+A LP M          R  G IV V ++ G   G P  +  Y+ASK A   F
Sbjct:   147 TGTFNLTQAALPAMKKFSDAAAKKRFVGTIVNVASVAGSTMGSPGSQAAYSASKAAVESF 206

Query:   202 FDCLRAEVEEYDVVISTV 219
               L  E+  Y   ++ V
Sbjct:   207 TKSLAMELSPYSASVAMV 224
```

Fig. 10

Input file Fbh25964Fl.seq; Output File 25964.trans
Sequence length 1725

GAGAAGGAGGAGCCAGCGGAAGGACGGTGTGCGGGCCGGCCAGCCCTGGACGAAAGAAGAGGGCCCCTCCAGGCCAGTC

TGGGCACCCTGGGATAGCGGCTGCAGCCATCAGCAGGGGCAGACGGCAGGTGGCCTGGTTGCTGCAGCTCCCAGGATCA

GCTCTGCCCTCCCCGCAAACGCCAGCCTCGTCACCGCTCCAGGGCACCTCCAGCAGTAACAGGTGGTTGCAGCAGGTGG

```
                                                  M   A   D   S   A   Q   A   Q   K      9
CAGCCAGCCCCTGGATGAGCCAAGGTCTCTTCCCCAGCCAGGC ATG GCC GAC TCT GCA CAG GCC CAG AAG     27

 L   V   Y   L   V   T   G   G   C   G   F   L   G   E   H   V   V   R   M   L      29
CTG GTG TAC CTG GTC ACA GGG GGC TGT GGC TTC CTG GGA GAG CAC GTG GTG CGA ATG CTG     87

 L   Q   R   E   P   R   L   G   E   L   R   V   F   D   Q   H   L   G   P   W      49
CTG CAG CGG GAG CCC CGG CTC GGG GAG CTG CGG GTC TTT GAC CAA CAC CTG GGT CCC TGG    147

 L   E   E   L   K   T   G   P   V   R   V   T   A   I   Q   G   D   V   T   Q      69
CTG GAG GAG CTG AAG ACA GGG CCT GTG AGG GTG ACT GCC ATC CAG GGG GAC GTG ACC CAG    207

 A   H   E   V   A   A   A   V   A   G   A   H   V   V   I   H   T   A   G   L      89
GCC CAT GAG GTG GCA GCA GCT GTG GCC GGA GCC CAT GTG GTC ATC CAC ACG GCT GGG CTG    267

 V   D   V   F   G   R   A   S   P   K   T   I   H   E   V   N   V   Q   G   T     109
GTA GAC GTG TTT GGC AGG GCC AGT CCC AAG ACC ATC CAT GAG GTC AAC GTG CAG GGT ACC    327

 R   N   V   I   E   A   C   V   Q   T   G   T   R   F   L   V   Y   T   S   S     129
CGG AAC GTG ATC GAG GCT TGT GTG CAG ACC GGA ACA CGG TTC CTG GTC TAC ACC AGC AGC    387

 M   E   V   V   G   P   N   T   K   G   H   P   F   Y   R   G   N   E   D   T     149
ATG GAA GTT GTG GGG CCT AAC ACC AAA GGT CAC CCC TTC TAC AGG GGC AAC GAA GAC ACC    447

 P   Y   E   A   V   H   R   H   P   Y   P   C   S   K   A   L   A   E   W   L     169
CCA TAC GAA GCA GTG CAC AGG CAC CCC TAT CCT TGC AGC AAG GCC CTG GCC GAG TGG CTG    507

 V   L   E   A   N   G   R   K   V   R   G   G   L   P   L   V   T   C   A   L     189
GTC CTG GAG GCC AAC GGG AGG AAG GTC CGT GGG GGG CTG CCC CTG GTG ACG TGT GCC CTT    567

 R   P   T   G   I   Y   G   E   G   H   Q   I   M   R   D   F   Y   R   Q   G     209
CGT CCC ACG GGC ATC TAC GGT GAA GGC CAC CAG ATC ATG AGG GAC TTC TAC CGC CAG GGC    627

 L   R   L   G   G   W   L   F   R   A   I   P   A   S   V   E   H   G   R   V     229
CTG CGC CTG GGA GGT TGG CTC TTC CGG GCC ATC CCG GCC TCT GTG GAG CAT GGC CGG GTC    687
```

Fig. 11A

```
 Y   V   G   N   V   A   W   M   H   V   L   A   A   R   E   L   E   Q   R   A    249
TAT GTG GGC AAT GTT GCC TGG ATG CAC GTG CTG GCA GCC CGG GAG CTG GAG CAG CGG GCA    747

 A   L   M   G   G   Q   V   Y   F   C   Y   D   G   S   P   Y   R   S   Y   E    269
GCC CTG ATG GGC GGC CAG GTA TAC TTC TGC TAC GAT GGA TCA CCC TAC AGG AGC TAC GAG    807

 D   F   N   M   E   F   L   G   P   C   G   L   R   L   V   G   A   R   P   L    289
GAT TTC AAC ATG GAG TTC CTG GGC CCC TGC GGA CTG CGG CTG GTG GGC GCC CGC CCA TTG    867

 L   P   Y   W   L   L   V   F   L   A   A   L   N   A   L   L   Q   W   L   L    309
CTG CCC TAC TGG CTG CTG GTG TTC CTG GCT GCC CTC AAT GCC CTG CTG CAG TGG CTG CTG    927

 R   P   L   V   L   Y   A   P   L   L   N   P   Y   T   L   A   V   A   N   T    329
CGG CCA CTG GTG CTC TAC GCA CCC CTG CTG AAC CCC TAC ACG CTG GCC GTG GCC AAC ACC    987

 T   F   T   V   S   T   D   K   A   Q   R   H   F   G   Y   E   P   L   F   S    349
ACC TTC ACC GTC AGC ACC GAC AAG GCT CAG CGC CAT TTC GGC TAT GAG CCC CTG TTC TCG   1047

 W   E   D   S   R   T   R   T   I   L   W   V   Q   A   A   T   G   S   A   Q    369
TGG GAG GAT AGC CGG ACC CGC ACC ATT CTC TGG GTA CAG GCC GCT ACG GGT TCA GCC CAG   1107

 *                                                                                370
TGA                                                                              1110

CGGTGGGGCTGGGGCCTGGAGGCCCAGATACAGCACATCCACCCAGGTCCCGAGCCCTCACACCCTGGACGGGAAGGGA

CAGCTGCATTCCAGAGCAGGAGGCAGGGCTCTGGGGCCAGAATGGCTGTCCTTGTCGTAGAGCCCTCCACATTTTCTTT

TTCTTTTTTGAGACAGGGTCTTGCTCTGTCACCCAGACTGGAATGCAAGTGGTGTGANTCATAAGCTCACTNGMACCCT

YAANCCTTCTGGGTTCAAGCAATCCTTNCTNGCCTYAANCCTTCTNGAACAAGCTTGGGANCCACAGGTGCACGCCANC

CACANCCTGGCTTTTTTTT
```

Fig. 11B

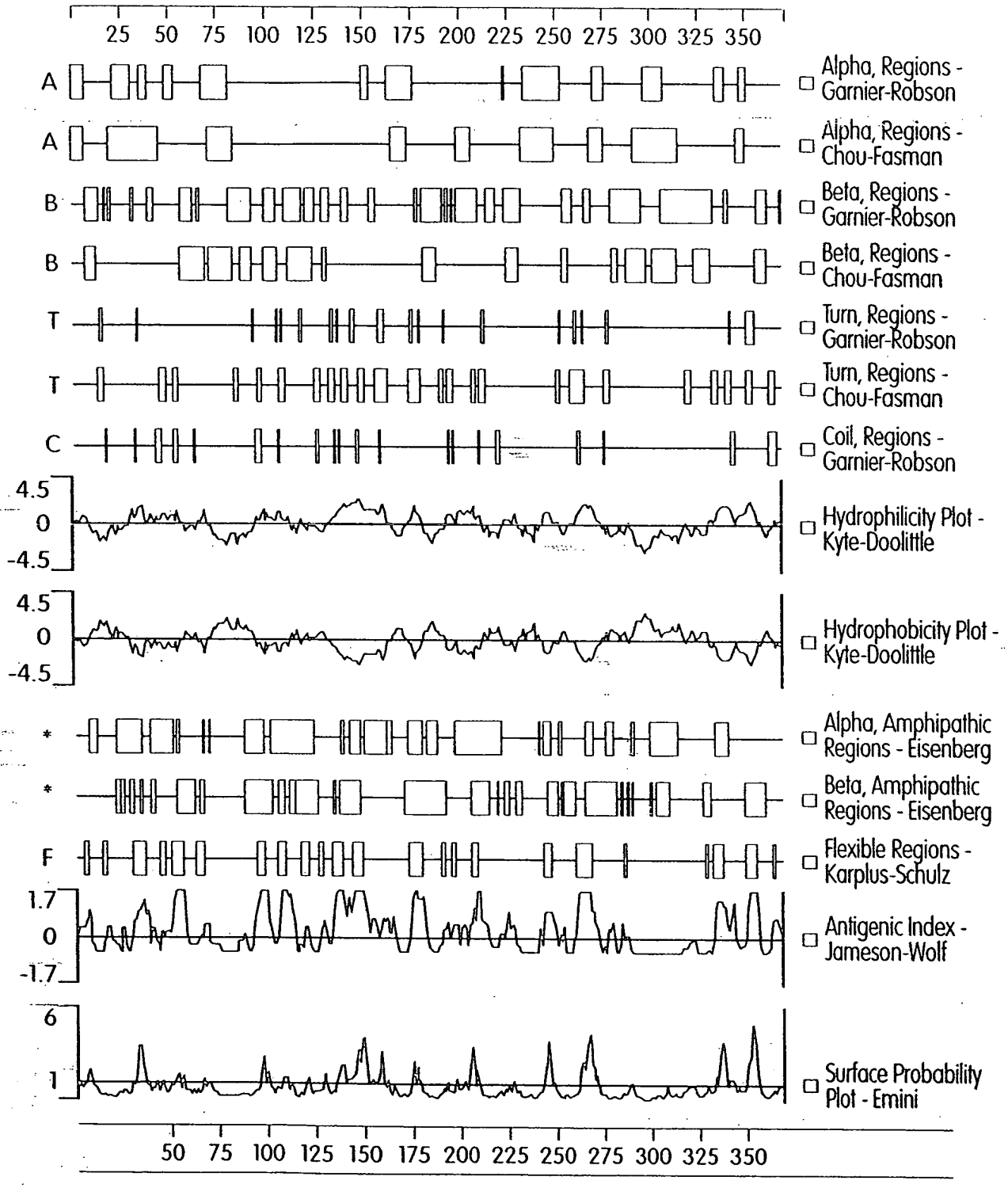

Fig. 12

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
10	26	out-->ins	1.0
73	90	ins-->out	2.0
289	305	out-->ins	3.0
312	333	ins-->out	1.2

>25964
MADSAQAQKLVYLVTGGCGFLGEHVVRMLLQREPRLGELRVFDQHLGPWLEELKTGPVRV
TAIQGDVTQAHEVAAAVAGAHVVIHTAGLVDVFGRASPKTIHEVNVQGTRNVIEACVQTG
TRFLVYTSSMEVVGPNTKGHPFYRGNEDTPYEAVHRHPYPCSKALAEWLVLEANGRKVRG
GLPLVTCALRPTGIYGEGHQIMRDFYRQGLRLGGWLFRAIPASVEHGRVYVGNVAWMHVL
AARELEQRAALMGGQVYFCYDGSPYRSYEDFNMEFLGPCGLRLVGARPLLPYWLLVFLAA
LNALLQWLLRPLVLYAPLLNPYTLAVANTTFTVSTDKAQRHFGYEPLFSWEDSRTRTILW
VQAATGSAQ

Fig. 13

Protein Family / Domain Matches, HMMer Version 2

```
Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:                 /prod/ddm/seqanal/PFAM/pfam5.0/Pfam
Sequence file:            /prod/ddm/wspace/orfanal/oa-script.9289.seq
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
 Query:  25964

Scores for sequence family classification (score includes all domains):
Model         Description                                   Score    E-value  N
--------      -----------                                   -----    ------- ---
3Beta_HSD      3-beta hydroxysteroid dehydrogenase/iso      676.9      1e-199  1
S-AdoMet_synt  S-adenosylmethionine synthetase               1.8        0.78  1
adh_short      short chain dehydrogenase                   -48.6       0.022  1
Epimerase      NAD dependent epimerase/dehydratase fam     -148.0      0.0016  1

Parsed for domains:
Model         Domain  seq-f seq-t    hmm-f hmm-t       score  E-value
--------      ------- ----- -----    ----- -----       -----  -------
adh_short       1/1      10   197 ..     1   203 []   -48.6    0.022
S-AdoMet_synt   1/1     341   351 ..   365   376 .]     1.8     0.78
3Beta_HSD       1/1       1   365 [.     1   425 []   676.9    1e-199
Epimerase       1/1      12   365 ..     1   359 []  -148.0   0.0016

Alignments of top-scoring domains:
adh_short: domain 1 of 1, from 10 to 197: score -48.6, E = 0.022
                   *->KvaLvlGassGIGlaiAkrLakeGakVvvadrneeklekGavalelk
                       v LvTG+++ +G  +++ L+ +     ++ ++  +   G +++elk
         25964     10    LVYLVTGGCGFLGEHVVRMLLQR--EPRLGELRVFDQHLGPWLEELK 54

                   elGgndkdralaiqlDvtdeesv.aaveqaverlGrlDvLVNNAGgiill
                     +     r+ aiq+Dvt++ +v aav+ a       +v++  AG  +
         25964     55 TGPV----RVTAIQGDVTQAHEVaAAVAGA-------HVVIHTAG--L-- 89

                   rpgpfaelsrtmeedwdrvidvNltgvflltravlplmamkkrggGrIvN
                    +  f + s   ++    +++vN+ g    tr v++  a ++ g    v
         25964     90 -VDVFGRAS---PK---TIHEVNVQG----TRNVIE--ACVQTGTRFLVY 126

                   iSSvaGrke.............g.glvgvpggsaYsASKaAvigltrs
                   +SS    +e  ++++++++  +++ +  +   ++ +Y +SKa    l++
         25964    127 TSS----MEvvgpntkghpfyrgnEdTPYEAVHRHPYPCSKA----LAEW 168

                   LAlElaphgIr......VnavaPGgvdTd<-*
                   L lE   +++r++ +    a  P g++ +
         25964    169 LVLEANGRKVRgglplvTCALRPTGIYGE    197

S-AdoMet_synt: domain 1 of 1, from 341 to 351: score 1.8, E = 0.78
                   *->HFGreevdFpWE<-*
                      HFG e   F+WE
         25964    341    HFGYEP-LFSWE    351
```

Fig. 14A

```
3Beta_HSD: domain 1 of 1, from 1 to 365: score 676.9, E = 1e-199
                *->elsesldmaglsclVTGGgGFlGrhIVreLlregeslqevRvfDlrf
                    +++s++   l++lVTGG+GFlG+h Vr+Ll+++++l e+RvfD +
25964      1    -MADSAQAQKLVYLVTGGCGFLGEHVVRMLLQREPRLGELRVFDQHL 46

                spelde.dssklqvitkikyieGDvtDkqdlaaAlqgiSCCTLLDmTLmD
                +p+l+e +++++ v+     +i+GDvt+++++aaA++g+
25964     47 GPWLEElKTGPVRVT----AIQGDVTQAHEVAAAVAGA---------- 80

                dvvIHtAaiiDvfGelrvsGSDLSFGVTVLFLAVTEGSYVVFYmGATDLR
                +vvIHtA+++DvfG
25964     81 HVVIHTAGLVDVFG---------------------------------- 94

                kasrdrimkVNVkGTqnvldACveaGVrvlVYTSSmeVVGpNsrGqpivN
                 as+ +i++VNV+GT+nv++ACv++G+r+lVYTSSmeVVGpN +G+p+++
25964     95 RASPKTIHEVNVQGTRNVIEACVQTGTRFLVYTSSMEVVGPNTKGHPFYR 144

                GdEttpYestDDhqdaYpeSKalAEklVLkANGsmlknGgrLyTCALRPa
                G+E+tpYe++  h+++Yp+SKalAE lVL+ANG+ +++G  L+TCALRP+
25964    145 GNEDTPYEAV--HRHPYPCSKALAEWLVLEANGRKVRGGLPLVTCALRPT 192

                gIfGeGdqflvpflrqlvknGlakfriGdknalsdrVYVgNVAwAHILAA
                gI+GeG q + +f+rq +++G+ +fr     ++ + rVYVgNCAw+H+LAA
25964    193 GIYGEGHQIMRDFYRQGLRLGGWLFRAIPASVEHGRVYVGNVAWMHVLAA 242

                raLqdpkkGREGassiaGqaYFIsDdsPvnSYddFnrtllkalGlrlpst
                r+L+++       a+ + Gq+YF++D+sP++SY+dFn+++l ++Glrl +
25964    243 RELEQR------AALMGGQVYFCYDGSPYRSYEDFNMEFLGPCGLRLVGA 286

                w.rlPlpllyvlaylnellswLLrklalrYtPllnpytvtlanttFtfst
                 ++lP++ll++la+ln+ll+wLLr+l + Y Pllnpyt+++anttFt+st
25964    287 RpLLPYWLLVFLAALNALLQWLLRPL-VLYAPLLNPYTLAVANTTFTVST 335

                nKAkkdLGYePlvtwEEarakTieWiqele<-*
                +KA++++GYePl++wE +r +Ti+W+q+
25964    336 DKAQRHFGYEPLFSWEDSRTRTILWVQAAT    365
```

Fig. 14B-1

```
Epimerase: domain 1 of 1, from 12 to 365: score -148.0, E = 0.0016
                *->ILVTGGAGFIGShlvreLlnn...ygddkVvvLDnLtdyYqyagnea
                   +LVTGG GF G h+vr Li+ +++ g  +V     +       + +
      25964    12    YLVTGGCGFLGEHVVRMLLQReprLGELRV-----FD----QHLGPW 49

                   rlevvegaprytFvkGDIcDrdlldkvfaehqpDaViHfAAeshV.drSi
                   ++e + g  r+t ++GD+  +  +  ++a     +ViH A++  V +r
      25964    50 LEELKTGPVRVTAIQGDVTQAHEVAAAVAGA--HVVIHTAGLVDVfGR-- 95

                   ekPlayidtNvvGTltLLEaaRnYWsaLdetkagvkkfvfsSTdeVYGdl
                     P +  + Nv GT + +Ea+             g   +v+ S+ eV G +
      25964    96 ASPKTIHEVNVQGTRNVIEACV---------QTGTRFLVYTSSMEVVGPN 136

                   esiPisaF...tEdtPynPs..SPYgaSKassEllvrayhraygLpaiiL
                   ++  +  F ++ EdtPy   ++ PY  SKa  E lv   +
      25964   137 TKGHP--FyrgNEDTPYEAVhrHPYPCSKALAEWLVLEAN---------- 174

                   RyFNvYGpyqsgriGedpngfpekLIPliiqnalgkgeplpvYGdDYpTp
                         G+   g+             +Pl+ + al    p  +YG
      25964   175 ------GRKVRGG-----------LPLV-TCALR---PTGIYG------ 196

                   DGtqv.RDw.....................ihVeDharANhllaltkg
                   +G q+ RD+ +++ + ++   +  + + ++++++V ++a   h+la +++
      25964   197 EGHQImRDFyrqglrlggwlfraipasvehgrVYVGNVAWM-HVLAAREL 245

                   ....................................raGkgsevYNiGg
                   +++    +++     ++++ ++ ++ + +  ++ + + +G
      25964   246 eqraalmggqvyfcydgspyrsyedfnmeflgpcglrLVG---------- 285

                   gneysnlEvVeaIekllgelaPekphvkakedpatfvddRpGddarya..
                     +  + + + +++++l+ 1          + ++ +++     ++++a
      25964   286 -ARPLLPYWLLVFLAALNALLQWL-----LRPLVLYAPLLN--PYTLAva 327

                   .....aDasKikreLGWkPevtnleeGladTvnWylene<-*
                   +++ +++ +K++I  G++P +   e+   +T+ W  +
      25964   328 nttftVSTDKAQRHFGYEPLFS-WEDSRTRTILWVQAAT    365
```

Fig 14B-2

ProdomId	Start	End	Description	Score
View Prodom 1280 Boxer ▼ Showing match ▼ Go!	11	362	p99.2 (39) 3BHS(5) 3BH1(4) 3BH2(3) // DEHYDROGENASE STEROID BETA-HYDROXYSTEROID 3BETA-HSD DEHYDROGENASE/DELTA 5-->4-ISOMERASE INCLUDES: PROGESTERONE 3-BETA-HYDROXY-DELTA5-STEROID 3-BETA-HYDROXY-5-ENE	395
ProdomId	Start	End	Description	Score

View Prodom 1280 Boxer ▼ Showing match ▼ Go!

```
>1280 p99.2 (39) 3BHS(5) 3BH1(4) 3BH2(3)  // DEHYDROGENASE STEROID
      BETA-HYDROXYSTEROID 3BETA-HSD DEHYDROGENASE/DELTA 5-->4-ISOMERASE
      INCLUDES: PROGESTERONE 3-BETA-HYDROXY-DELTA5-STEROID 3-BETA-HYDROXY-5-ENE
      Length = 416

 Score = 395 (144.1 bits), Expect = 3.2e-42, Sum P(2) = 3.2e-42
 Identities = 99/268 (36%), Positives = 134/268 (50%)

Query:   102 HEVNVQGTRNVIEACVQTGTRFLVYTSSMEVVGPNTKGHPFYRGNEDTPYEAVHRHPYPC 161
             ++ NVQGTRN+IE C      RF       MEV GPN+        G+E+  +E+    +PYP
Sbjct:   157 YKFNVQGTRNLIEKC-----RFF---GVMEVAGPNSYKEIILNGHEEEHHESTWPNPYPY 208

Query:   162 -SKALAEWLVLEANGRKVRGGLPLVTCALRPTGIYGEGHQIMRDFYRQGLRLGGWLFRAI 220
              SK +AE  VL ANG  ++ G  L TCALRP  IYGEG + +      Q L+ GG +FR
Sbjct:   209 YSKKMAEKAVLAANGSMLKNGGTLYTCALRPMYIYGEGDKFLSPMIVQALKNGGIMFRVG 268

Query:   221 PASVEHGRVYVGNVAWMHVXXXXXXXXXXXX--MGGQVYFCYDGSPYRSYEDFNMEFLGP 278
                       VYVGNVAW H+                + GQ Y+  D +P++SY+D N
Sbjct:   269 GKFSVANPVYVGNVAWAHILAARGLQDPKKSPNIQGQFYYISDDTPHQSYDDLNYTLSKE 328

Query:   279 CGLRLVGARPLLP----YWXXXXXXXXXXXXXXXXXXXXXXXXXNPYTLAVANTTFTVS 334
              GLRL  ++  LP    YW                              N + + ++NTTFT S
Sbjct:   329 WGLRLDSSKWRLPLPLLYWLAFLLEMVSFLLRPISYNYQPPF---NRHLVTLSNTTFTFS 385

Query:   335 TDKAQRHFGYEPLFSWEDSRTRTILWVQ 362
               KAQR  GYEPL SWE+++ +T  W++
Sbjct:   386 YKKAQRDLGYEPLVSWEEAKQKTSEWIE 413

 Score = 65 (27.9 bits), Expect = 3.2e-42, Sum P(2) = 3.2e-42
 Identities = 11/23 (47%), Positives = 17/23 (73%)

Query:    11 VYLVTGGCGFLGEHVVRMLLQRE 33
             VY VTGG  FLG ++V++L+  +
Sbjct:    14 VYAVTGGAEFLGRYIVKLLISAD 36
```

Fig. 15

Input file Fbh21686Fl.seq; Output File 21686.trans
Sequence length 1209

```
                                                                  M   S   L   R        4
CCCACGCGTCCGCCCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCGCCCGCCTCGA ATG TCC CTG AGA       12

 P   R   R   A   C   A   Q   L   L   W   H   P   A   A   G   M   A   S   W   A    24
CCC AGA AGG GCC TGC GCT CAG CTG CTC TGG CAC CCC GCT GCA GGG ATG GCC TCC TGG GCT    72

 K   G   R   S   Y   L   A   P   G   L   L   Q   G   Q   V   A   I   V   T   G    44
AAG GGC AGG AGC TAC CTG GCG CCT GGT TTG CTG CAG GGC CAA GTG GCC ATC GTC ACC GGC   132

 G   A   T   G   I   G   K   A   I   V   K   E   L   L   E   L   G   S   N   V    64
GGG GCC ACG GGC ATC GGA AAA GCC ATC GTG AAG GAG CTC CTG GAG CTG GGG AGT AAT GTG   192

 V   I   A   S   R   K   L   E   R   L   K   S   A   A   D   E   L   Q   A   N    84
GTC ATT GCA TCC CGT AAG TTG GAG AGA TTG AAG TCT GCG GCA GAT GAA CTG CAG GCC AAC   252

 L   P   P   T   K   Q   A   R   V   I   P   I   Q   C   N   I   R   N   E   E   104
CTA CCT CCC ACA AAG CAG GCA CGA GTC ATT CCC ATA CAA TGC AAC ATC CGG AAT GAG GAG   312

 E   V   N   N   L   V   K   S   T   L   D   T   F   G   K   I   N   F   L   V   124
GAG GTG AAT AAT TTG GTC AAA TCT ACC TTA GAT ACT TTT GGT AAG ATC AAT TTC TTG GTG   372

 N   N   G   G   G   Q   F   L   S   P   A   E   H   I   S   S   K   G   W   H   144
AAC AAT GGA GGA GGC CAG TTT CTT TCC CCT GCT GAA CAC ATC AGT TCT AAG GGA TGG CAC   432

 A   V   L   E   T   N   L   T   G   T   F   Y   M   C   K   A   V   Y   S   S   164
GCT GTG CTT GAG ACC AAC CTG ACG GGT ACC TTC TAC ATG TGC AAA GCA GTT TAC AGC TCC   492

 W   M   K   E   H   G   G   S   I   V   N   I   I   V   P   T   K   A   G   F   184
TGG ATG AAA GAG CAT GGA GGA TCT ATC GTC AAT ATC ATT GTC CCT ACT AAA GCT GGA TTT   552

 P   L   A   V   H   S   G   A   A   R   A   G   V   Y   N   L   T   K   S   L   204
CCA TTA GCT GTG CAT TCT GGA GCT GCA AGA GCA GGT GTT TAC AAC CTC ACC AAA TCT TTA   612

 A   L   E   W   A   C   S   G   I   R   I   N   C   V   A   P   G   V   I   Y   224
GCT TTG GAA TGG GCC TGC AGT GGA ATA CGG ATC AAT TGT GTT GCC CCT GGA GTT ATT TAT   672

 S   Q   T   A   V   E   N   Y   G   S   W   G   Q   S   F   F   E   G   S   F   244
TCC CAG ACT GCT GTG GAG AAC TAT GGT TCC TGG GGA CAA AGC TTC TTT GAA GGG TCT TTT   732

 Q   K   I   P   A   K   R   I   G   V   P   E   E   V   S   S   V   V   C   F   264
CAG AAA ATC CCC GCT AAA CGA ATT GGT GTT CCT GAG GAG GTC TCC TCT GTG GTC TGC TTC   792

 L   L   S   P   A   A   S   F   I   T   G   Q   S   V   D   V   D   G   G   R   284
CTA CTG TCT CCT GCA GCT TCC TTC ATC ACT GGA CAG TCG GTG GAT GTG GAT GGG GGC CGG   852

 S   L   Y   T   H   S   Y   E   V   P   D   H   D   N   W   P   K   G   A   G   304
AGT CTC TAT ACT CAC TCG TAT GAG GTA CCA GAT CAT GAC AAC TGG CCC AAG GGA GCA GGG   912

 D   L   S   V   V   K   K   M   K   E   T   L   K   E   K   A   K   L   *       323
GAC CTT TCT GTT GTC AAA AAG ATG AAG GAG ACC TTA AAG GAG AAA GCT AAG CTC TGA       969

GCTGAGGAAACAAGGTGTCCTCCATCCCCAGTGCCTTCACATCTTGAGGATATGCTTCTGTACTTTTTAAAAGCTTATA

GTTGGTATGGAAAACATTTTTCTTATTTTTAAGTGTTATTAATTATATCTATGGAAAAACTATTCCTGAAATATATACA

GTCTTATGTCCCAAAAAAAAAA
```

Fig. 16

CLUSTAL W (1.74) multiple sequence alignment

```
5052204_SDR_rat ----------MGSWKSGQSYLAAGLLQNQVAVVTGGATGIGKAISRELLHL
21686           MSLRPRRACAQLLWHPAAGMASWAKGRSYLAPGLLQGQVAIVTGGATGIGKAIVKELLEL
                          *.** .*:****.****.***:************ :***.*

5052204_SDR_rat GCNVVIASRKLDRLTAAVDELRASQPPSSSTQVTAIQCNIRKEEEVNNLVKSTLAKYGKI
21686           GSNVVIASRKLERLKSAADELQANLPPTKQARVIPIQCNIRNEEEVNNLVKSTLDTFGKI
                *.*********:**.:*.***:*. **:..::* .******:************ .:***

5052204_SDR_rat NFLVNNAGGQFMAPAEDITAKGWQAVIETNLTGTFYMCKAVYNSWMKDHGGSIVNIIVLL
21686           NFLVNNGGGQFLSPAEHISSKGWHAVLETNLTGTFYMCKAVYSSWMKEHGGSIVNIIVPT
                ******.****::***.*::***:**:***************.****:**********

5052204_SDR_rat NNGFPTAAHSGAARAGVYNLTKTMALTWASSGVRINCVAPGTIYSQTAVDNYGELGQTMF
21686           KAGFPLAVHSGAARAGVYNLTKSLALEWACSGIRINCVAPGVIYSQTAVENYGSWGQSFF
                : *** *.***************::** **.**:********.*******:***. **::*

5052204_SDR_rat EMAFENIPAKRVGLPEEISPLVCFLLSPAASFITGQLINVDGGQALYTRNFTIPDHDNWP
21686           EGSFQKIPAKRIGVPEEVSSVVCFLLSPAASFITGQSVDVDGGRSLYTHSYEVPDHDNWP
                * :*::*****:*:***:*.:*************** ::****::***:.: :********

5052204_SDR_rat VGAGDSSFIKKVKESLKKQARL
21686           KGAGDLSVVKKMKETLKEKAKL
                 **** *.:**:**:**::*:*
```

Fig. 17

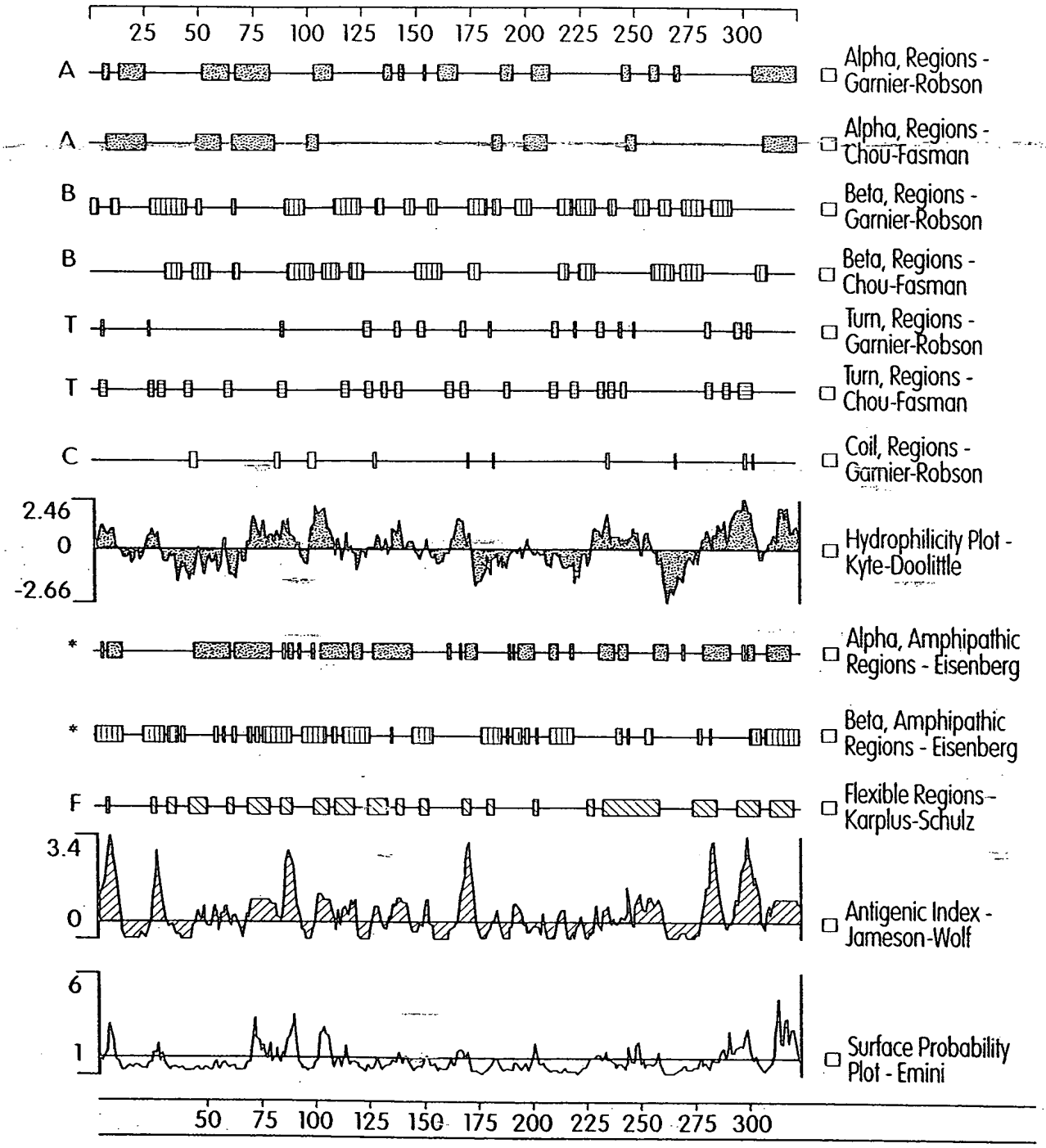

Fig. 18

Signal Peptide Predictions for 21686

Method	Predict	Score	Mat@
Signal (eukaryote)	MAYBE		20

Note: amino-terminal 70aa used for signal peptide prediction

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
29	50	ins-->out	0.9
170	188	out-->ins	0.2
208	224	ins-->out	0.6
258	275	out-->ins	2.6

>21686
MSLRPRRACAQLLWHPAAGMASWAKGRAYLAPGLLQGQVAIVTGGATGIGKAIVKELLEL
GSNVVIASRKLERLKSAADELQANLPPTKQARVIPIQCNIRNEEEVNNLVKSTLDTFGKI
NFLVNNGGGQFLSPAEHISSKGWHAVLETNLTGTFYMCKAVYSSWMKEHGGSIVNIIVPT
KAGFPLAVHSGAARAGVYNLTKSLALEWACSGIRINCVAPGVIYSQTAVENYGSWGQSFF
EGSFQKIPAKRIGVPEEVSSVVCFLLSPAASFITGQSVDVDGGRSLYTHSYEVPDHDNWP
KGAGDLSVVKKMKETLKEKAKL

Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
10	31	ins-->out	0.9
151	169	out-->ins	0.2
189	205	ins-->out	0.6
239	256	out-->ins	2.6

>21686_mature
MASWAKGRSYLAPGLLQGQVAIVTGGATGIGKAIVKELLELGSNVVIASRKLERLKSAAD
ELQANLPPTKQARVIPIQCNIRNEEEVNNLVKSTLDTFGKINFLVNNGGGQFLSPAEHIS
SKGWHAVLETNLTGTFYMCKAVYSSWMKEHGGSIVNIIVPTKAGFPLAVHSGAARAGNYN
LTKSLALEWACSGIRINCVAPGVIYSQTAVENYGSWGQSFFEGSFQKIPAKRIGVPEEVS
SVVCFLLSPAASFITGQSVDVDGGRSLYTHSYEVPDHDNWPKGAGDLSVVKKMKETLKEK
AKL

Fig. 19

Protein Family / Domain Matches, HMMer Version 2

```
Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:                 /prod/ddm/seqanal/PFAM/pfam4.4/Pfam
Sequence file:            /prod/ddm/wspace/orfanal/oa-script.19160.seq
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
 Query:   21686

Scores for sequence family classification (score includes all domains):
Model        Description                                   Score    E-value  N
--------     -----------                                   -----    ------- ---
adh_short    short chain dehydrogenase                     162.5    7.3e-45  1
adh_short_C2 short chain dehydrogenase/reductase C-te       47.2    3.7e-10  1

Parsed for domains:
Model        Domain  seq-f seq-t    hmm-f hmm-t       score  E-value
--------     ------- ----- -----    ----- -----       -----  -------
adh_short      1/1      38   226 ..     1   203 []    162.5  7.3e-45
adh_short_C2   1/1     250   280 ..     1    31 []     47.2  3.7e-10

Alignments of top-scoring domains:
adh_short: domain 1 of 1, from 38 to 226:  score 162.5, E = 7.3e-45
                   *->KvaLvTGassGIGlaiAkrLakeGakVvvadrneeklekGavakelk
                      +va+vTG++ GIG+ai+k+L++ G +Vv+a r  e+l     ++++
       21686    38    QVAIVTGGATGIGKAIVKELLELGSNVVIASRKLERL-----KSAAD 79

                      elGgnd....kdralaiqlDvtdeesv.aaveqaverlGrlDvLVNNAGg
                      el +n+++++  r+++iq++++ ee+v+++v+  ++ +G+++ LVNN Gg
       21686    80 ELQANLpptkQARVIPIQCNIRNEEEVnNLVKSTLDTFGKINFLVNNGGG 129

                      .iillrpgpfaelsrtmeedwdrvidvNltgvfllltravlplmamkkrgg
                      +++     p++ +s    + w +v+++Nltg+f++++av      +k +g
       21686   130 qFL----SPAEHIS---SKGWHAVLETNLTGTFYMCKAVYS--SWMKEHG 170

                      GrIvNiSSvaGrkegglvgvpggsaYsASKaAvigltrsLAlElaphgIr
                      G+IvNi          + g+p  ++ +A+ a+v  lt+sLAlE+a  gIr
       21686   171 GSIVNIIV-PT-----KAGFPLAVHSGAARAGVYNLTKSLALEWACSGIR 214

                      VnavaPGgvdTd<-*
                      +n+vaPG ++ +
       21686   215 INCVAPGVIYSQ    226

adh_short_C2: domain 1 of 1, from 250 to 280: score 47.2, E = 3.7e-10
                   *->gRlGePeEiAnavvFLASdaAsYiTGqtlvV<-*
                      +R G PeE++++v FL S+aAs+iTGq + V
       21686   250   KRIGVPEEVSSVVCFLLSPAASFITGQSVDV    280
```

Fig. 20

ProDom Matches

ProdomId	Start	End	Description	Score
View Prodom 121622 Boxer / Showing match / Go!	29	82	p99.2 (1) YSO5_CAEEL // HYPOTHETICAL 98.0 KD PROTEIN F56D1.5 IN CHROMOSOME II TRANSMEMBRANE	70
View Prodom 95301 Boxer / Showing match / Go!	35	82	p99.2 (1) O27957_ARCFU // SHIKIMATE 5-DEHYDROGENASE AROE HYPOTHETICAL PROTEIN	86
View Prodom 11 Boxer / Showing match / Go!	37	231	p99.2 (1078) ADH(34) GALE(20) FABG(13) // OXIDOREDUCTASE PROTEIN DEHYDROGENASE NAD REDUCTASE NADP BIOSYNTHESIS SYNTHASE ALCOHOL PUTATIVE	157
View Prodom 73753 Boxer / Showing match / Go!	237	286	p99.2 (1) P71079_BACSU // UNIDENTFIED DEHYDROGENASE	84
View Prodom 77223 Boxer / Showing match / Go!	243	287	p99.2 (1) O07882_STAXY // GLUCOSE-1-DEHYDROGENASE	92
ProdomId	Start	End	Description	Score

View Prodom 11 [Boxer] [Showing match] [Go!]

```
>11 p99.2 (1078) ADH(34) GALE(20) FABG(13)  // OXIDOREDUCTASE PROTEIN
    DEHYDROGENASE NAD REDUCTASE NADP BIOSYNTHESIA SYNTHASE ALCOHOL PUTATIVE
    Length = 269

 Score = 157 (60.3 bits), Expect = 1.2e-09, P = 1.2e-09
 Identities = 64/213 (30%), Positives = 106/213 (49%)

Query:    51 KAIVKELLELGSNVVIASRKLERLKSAADELQANLPPTKQA---RVIPIQCNIRNEEEVN 107
             K +V       S    AS+  E     +  + A +  T QA     V  + C++ + E+V
Sbjct:    35 KVVVVSATSEEGESTEASK--ESAMEVSKAVNAEVSATMQAVGVTVTKVTCDVADVEDVE 92

Query:   108 NLVKSTLDTF----GKINFLVNNGGGQFLSP---AEHISSKG-----WHAVLETNLTGTF 155
              LV++ ++ F    GKI+ LVNN G    ++P    AE ++ +       W  V+E N+TGTF
Sbjct:    93 KLVETVVEEFSGIHGKIDVLVNNAG--VMAPKAVAESMTEETSDDEEWEEVIEVNVTGTF 150

Query:   156 YMCKAVYSSWMK--------EHGGSIVNI--IVPTKAGFP--LAVHSGAARAGVYNLTKS 203
              + +A    +  K            G+IVN+   +   +  G P    A +S A++A V + TKS
Sbjct:   151 NLTQAALPAMKKFSDAAAKKRFVGTIVNVASVAGSTMGSPGSQAAYS-ASKAAVESFTKS 209

Query:   204 LALE---WACSG--IRINCVAPGVIYSQTAVEN 231
             LA+E    ++ S    +R+N VAPG + +  A+E+
Sbjct:   210 LAMELSPYSASVAMVRVNAVAPGYVETD-ALES 241

 Score = 103 (41.3 bits), Expect = 0.0021, Sum P(2) = 0.0021
 Identities = 32/100 (32%), Positives = 54/100 (54%)

Query:    37 GQVAIVTGGA--TGIGKAIVKELLELGSNVVIASRKLERLKS--AADE--------LQAN 84
             G+  +VTGG+  +GIG AI ++L E G+ VV+ S   E  +S  A+ E          + A
Sbjct:     7 GKTVLVTGGSGFSGIGLAIARQLAEEGAKVVVVSATSEESESTEASKESAMEVSKAVNAE 66

Query:    85 LPPTKQA---RVIPIQCNIRNEEEVNNLVKSTLDTFGKIN 121
             +  T QA     V  + C++ + E+V  LV++ ++ F  I+
Sbjct:    67 VSATMQAVGVTVTKVTCDVADVEDVEKLVETVVEEFSGIH 106

 Score = 37 (18.1 bits), Expect = 0.0021, Sum P(2) = 0.0021
 Identities = 9/23 (39%), Positives = 13/23 (56%)

Query:   205 ALEWACSGIRINCVAPGVIYSQT 227
             ALE A +G+ +  V PG +   T
Sbjct:   238 ALESATNGLSVVTVRPGNVRVNT 260
```

Fig. 21A

View Prodom 77223 [Boxer] [Showing match] [Go!]

```
>77223 p99.2 (1) O07882_STAXY // GLUCOSE-1-DEHYDROGENASE
       Length = 67

 Score = 92 (37.4 bits), Expect = 0.00031, P = 0.00031
 Identities = 19/45 (42%), Positives = 29/45 (64%)

Query:   243 SFQKIPAKRIGVPEEVSSVVCFLLSPAASFITGQSVDVDGGRSLY 287
            + + IPAK IG  ++V++V  FL S  A +I G ++ VDGG + Y
Sbjct:    15 TLEMIPAKEIGFADQVANVARFLCSDLADYIHGTTIYVDGGMTNY 59
```

View Prodom 95301 [Boxer] [Showing match] [Go!]

```
>95301 p99.2 (1) O27957_ARCFU // SHIKIMATE 5-DEHYDROGENASE
AROE HYPOTHETICAL
       PROTEIN
       Length = 108

 Score = 86 (35.3 bits), Expect = 0.0014, P = 0.0014
 Identities = 20/48 (41%), Positives = 31/48 (64%)

Query:    35 LQGQVAIVTGGATGIGKAIVKELLELGSNVVIASRKLERLKSAADELQ 82
             L G+ A+V G A G GKA    LL++GS V++A+R  E+ + A + L+
Sbjct:    10 LGGKTALVVG-AGGAGKAAAALALLDMGSTVIVANRTEEKGREAVEMLR 56
```

View Prodom 73753 [Boxer] [Showing match] [Go!]

```
>73753 p99.2 (1) P71079_BACSU // UNIDENTFIED DEHYDROGENASE
       Length = 60

 Score = 84 (34.6 bits), Expect = 0.0023, P = 0.0023
 Identities = 20/50 (40%), Positives = 29/50 (58%)

Query:   237 QSFFEGSFQKIPAKRIGVPEEVSSVVCFLLSPAASFITGQSVDVDGGRSL 286
            +  E + Q  PA R+   +++   V FL+S  A  I GQ++ VDGGRSL
Sbjct:     9 EDLLEDARQNTPAGRMVEIKDMVDTVEFLVSSKADMIRGQTIIVDGGRSL 58
```

View Prodom 121622 [Boxer] [Showing match] [Go!]

```
>121622 p99.2 (1) YSO5_CAEEL // HYPOTHETICAL 98.0 KD PROTEIN F56D1.5 IN
        CHROMOSOME II TRANSMEMBRANE
        Length = 194

 Score = 70 (29.7 bits), Expect = 7.6, P = 1.0
 Identities = 20/57 (35%), Positives = 29/57 (50%)

Query:    29 YLAPG;;QGQV--AIVTGGATGIGKAIVKELLELG-SNVVIASRKLERLKSAADELQ 82
             +  P L Q Q    +V+GG  GIGKA   EL + G    V+  R  ++L S   E++
Sbjct:    62 FYKPNLEQYQHRWTVVSGGTDGIGKAYTLELAKRGLRKFVLIGRNPKKLDSVKSEIE 118
```

Fig. 21B

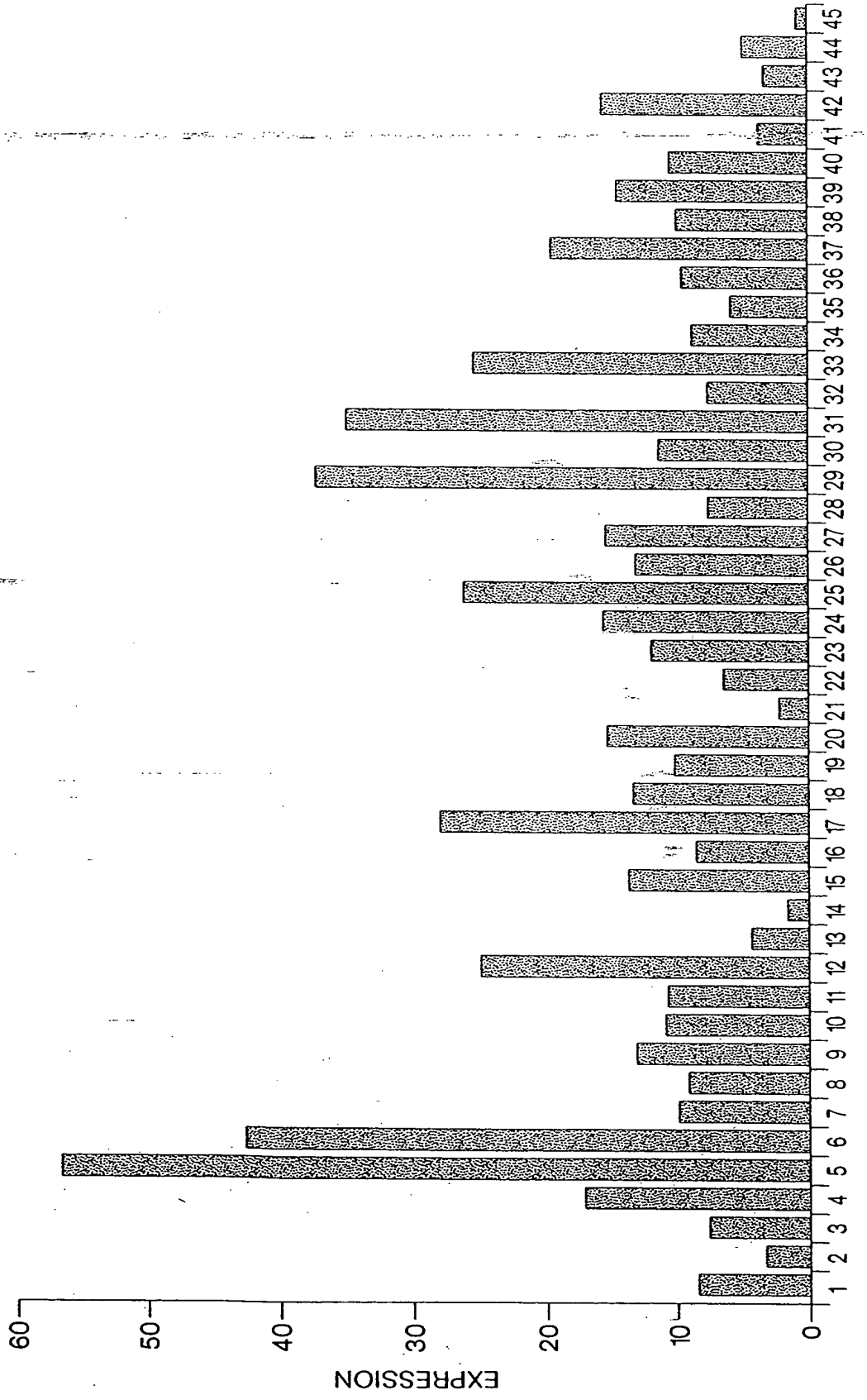

Fig. 22

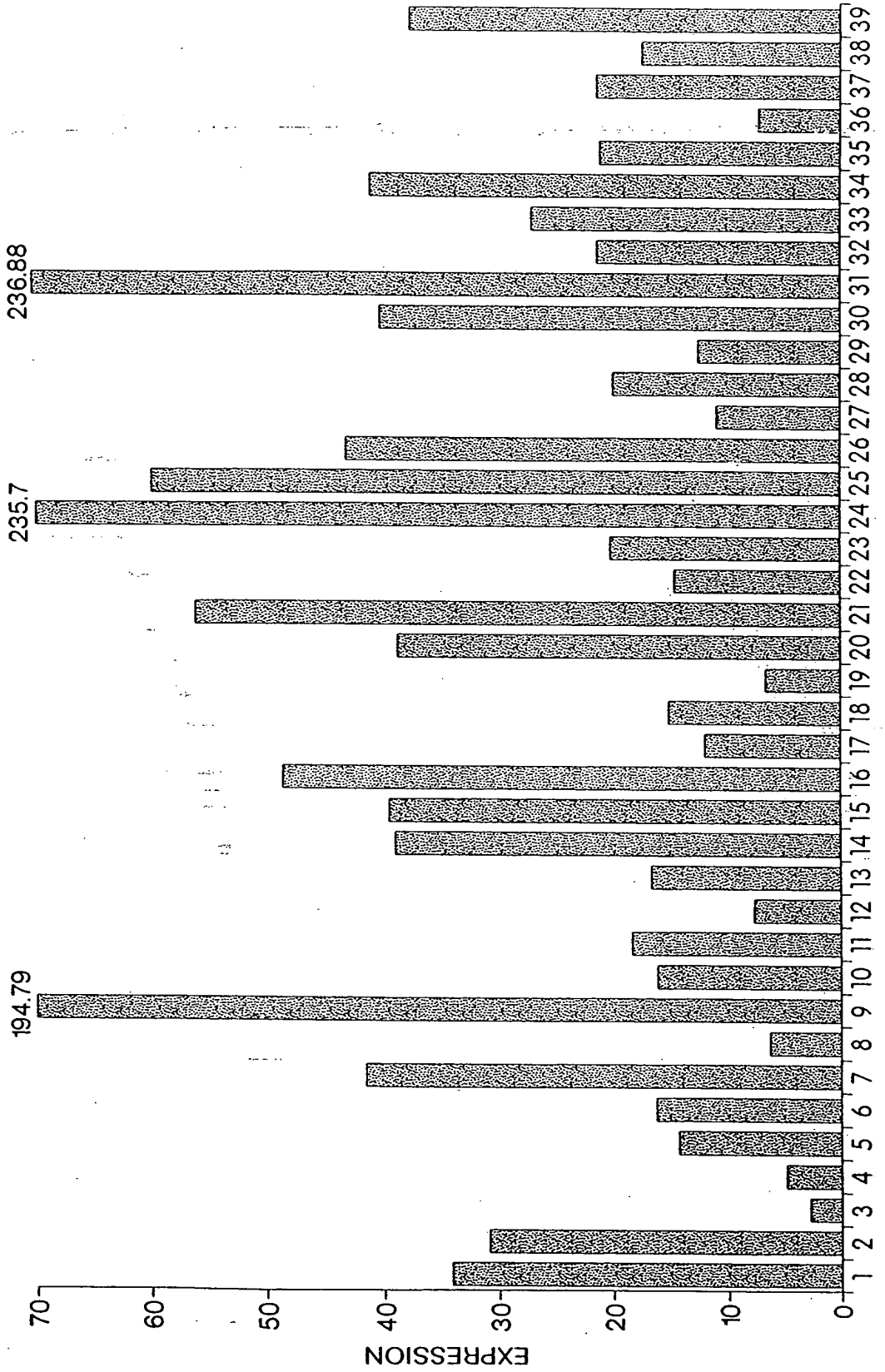

Fig. 23

Applicants: Rachel E. Meyers, et al.
Title: 21481, A NOVEL DEHYDROGENASE MOLECULE AND USES THEREFOR
Attorney/Agent: Kerri Pollard Schray
Docket No.: MPI00-079P1RCP2CN1M

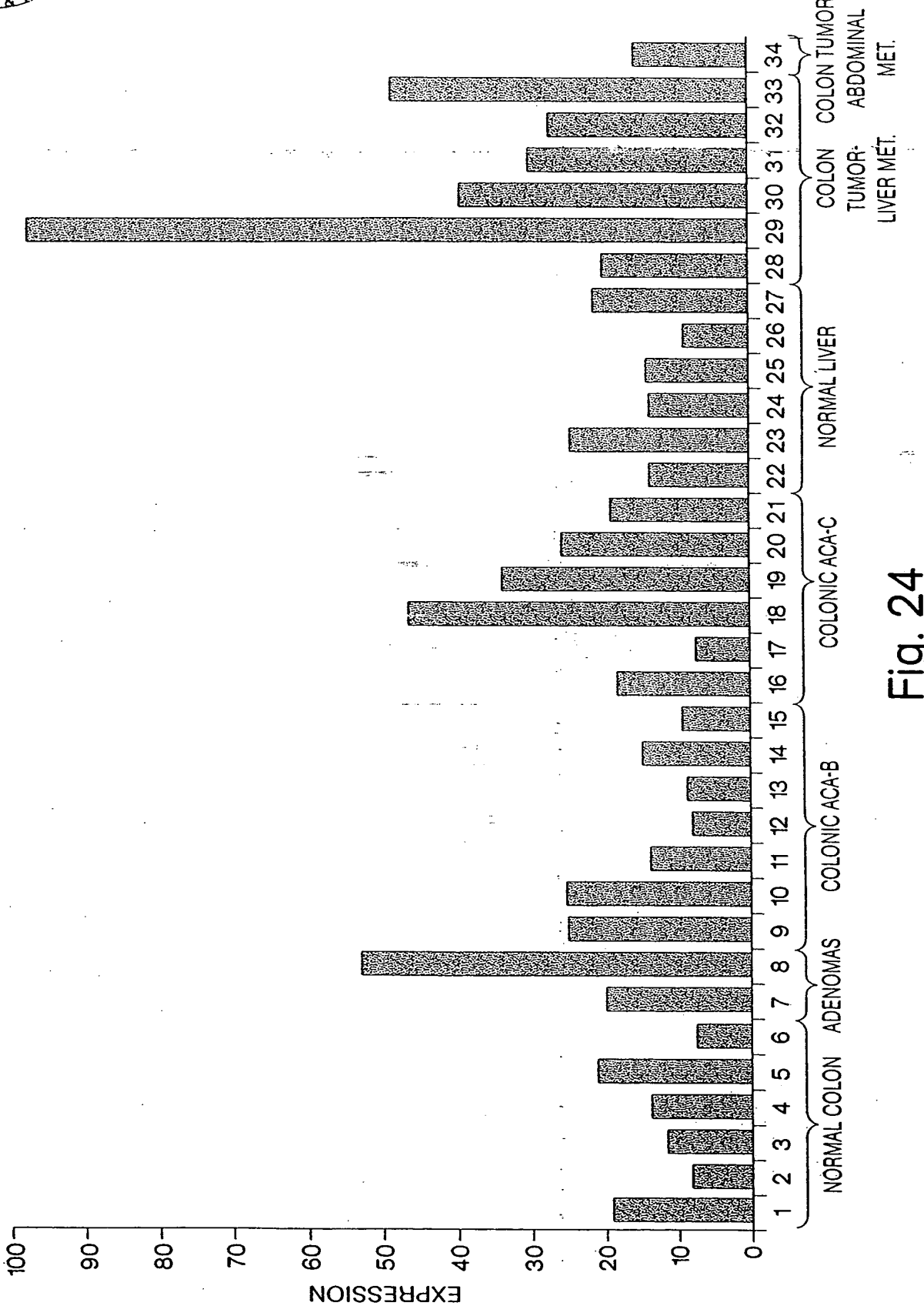

Fig. 24

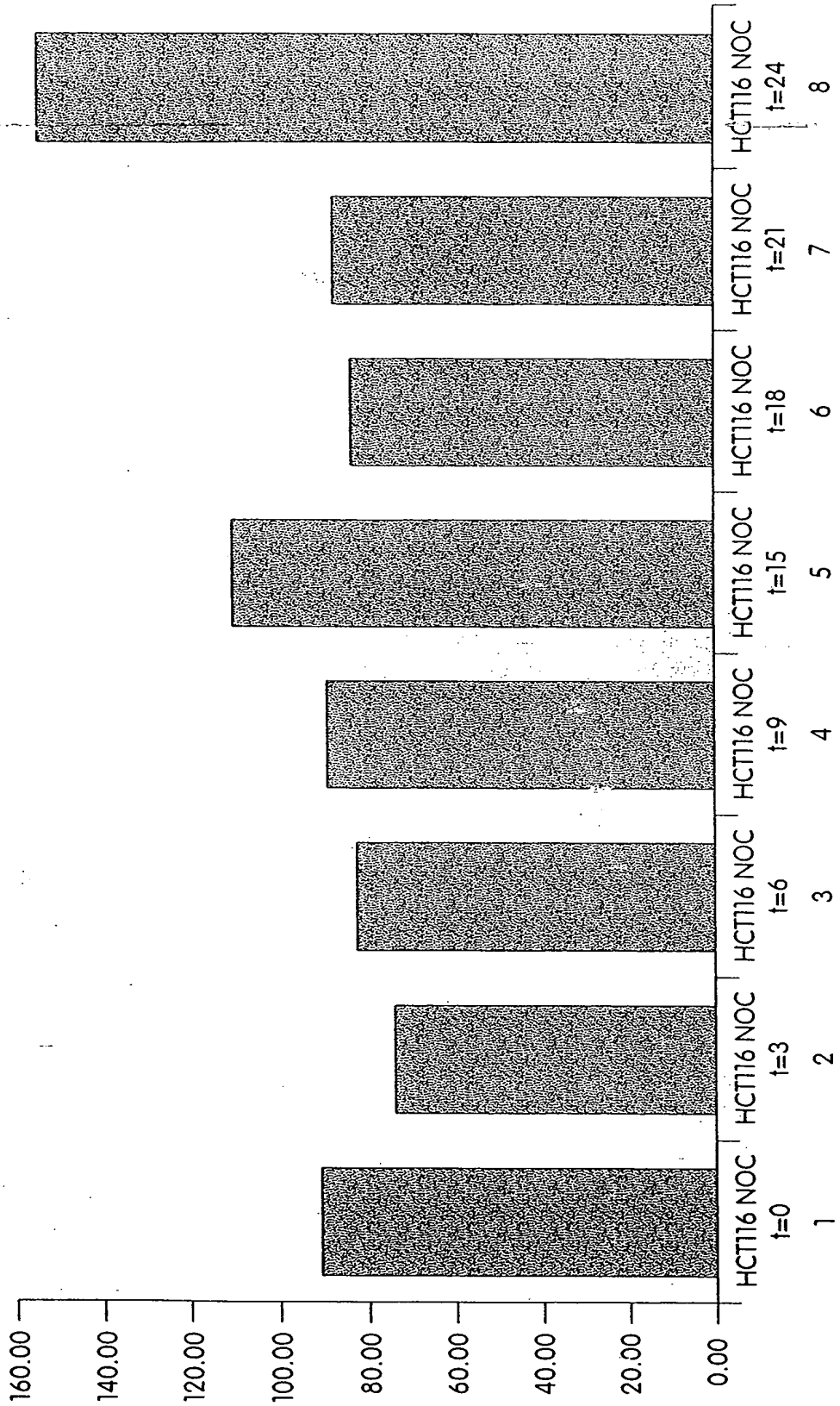

Fig. 25

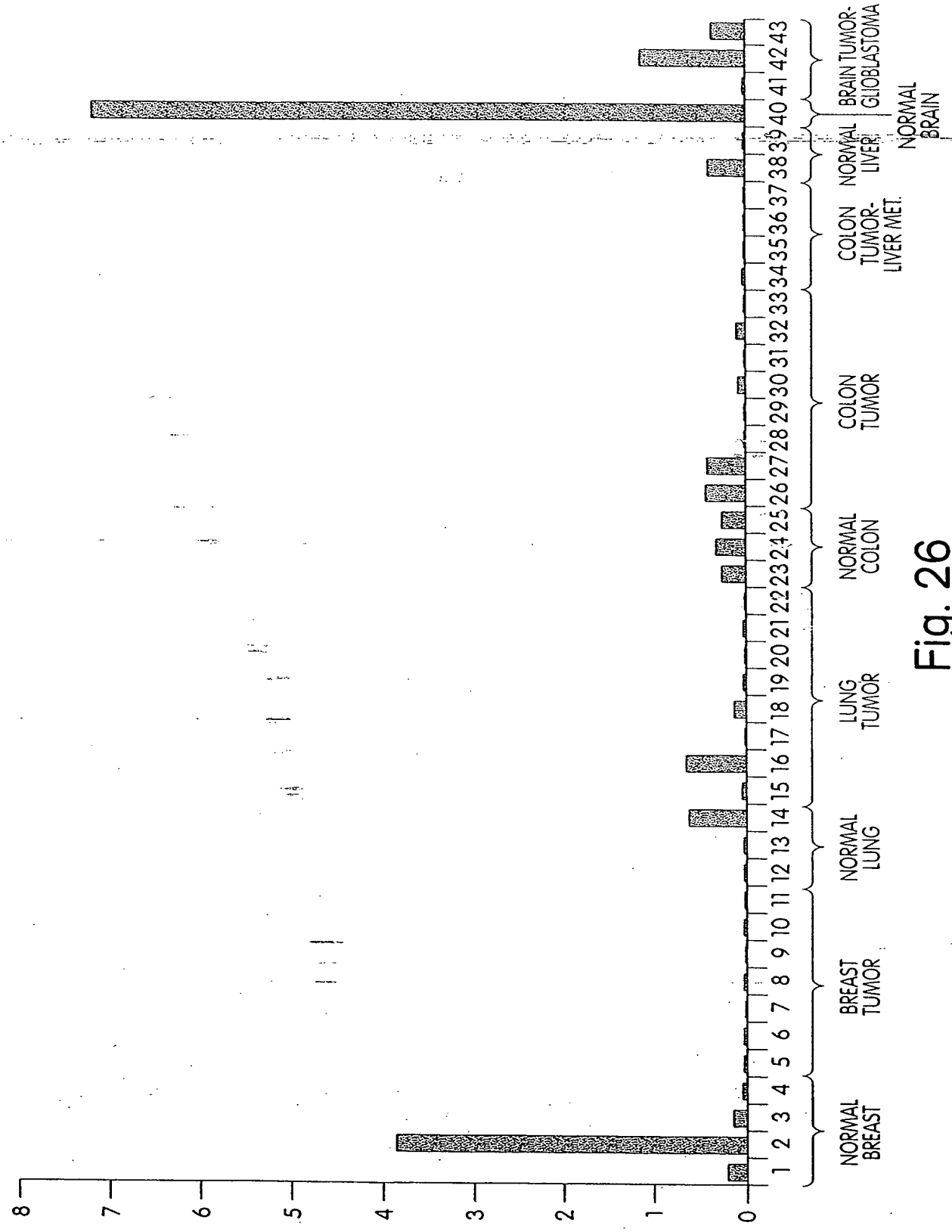

Fig. 26

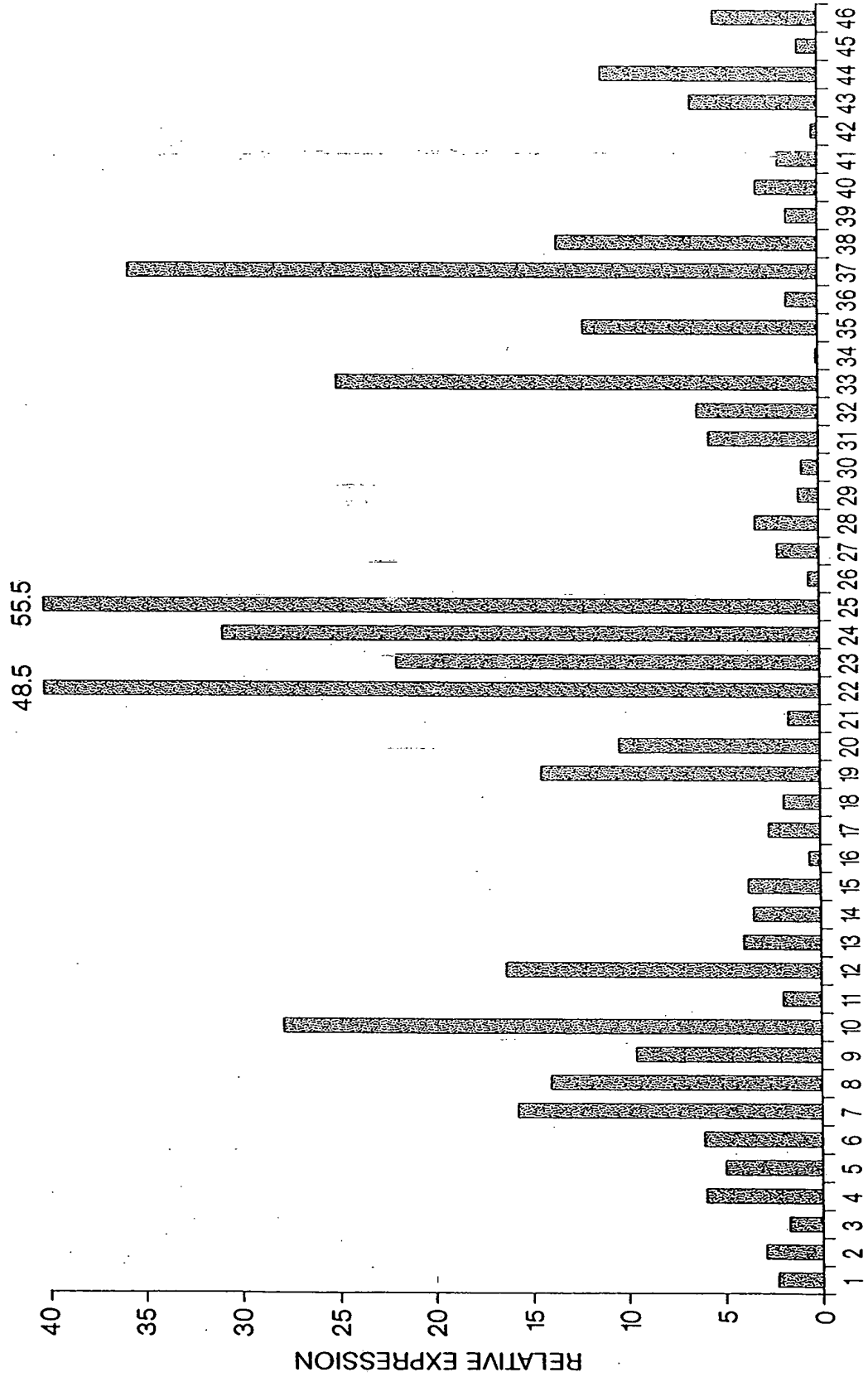

Fig. 27

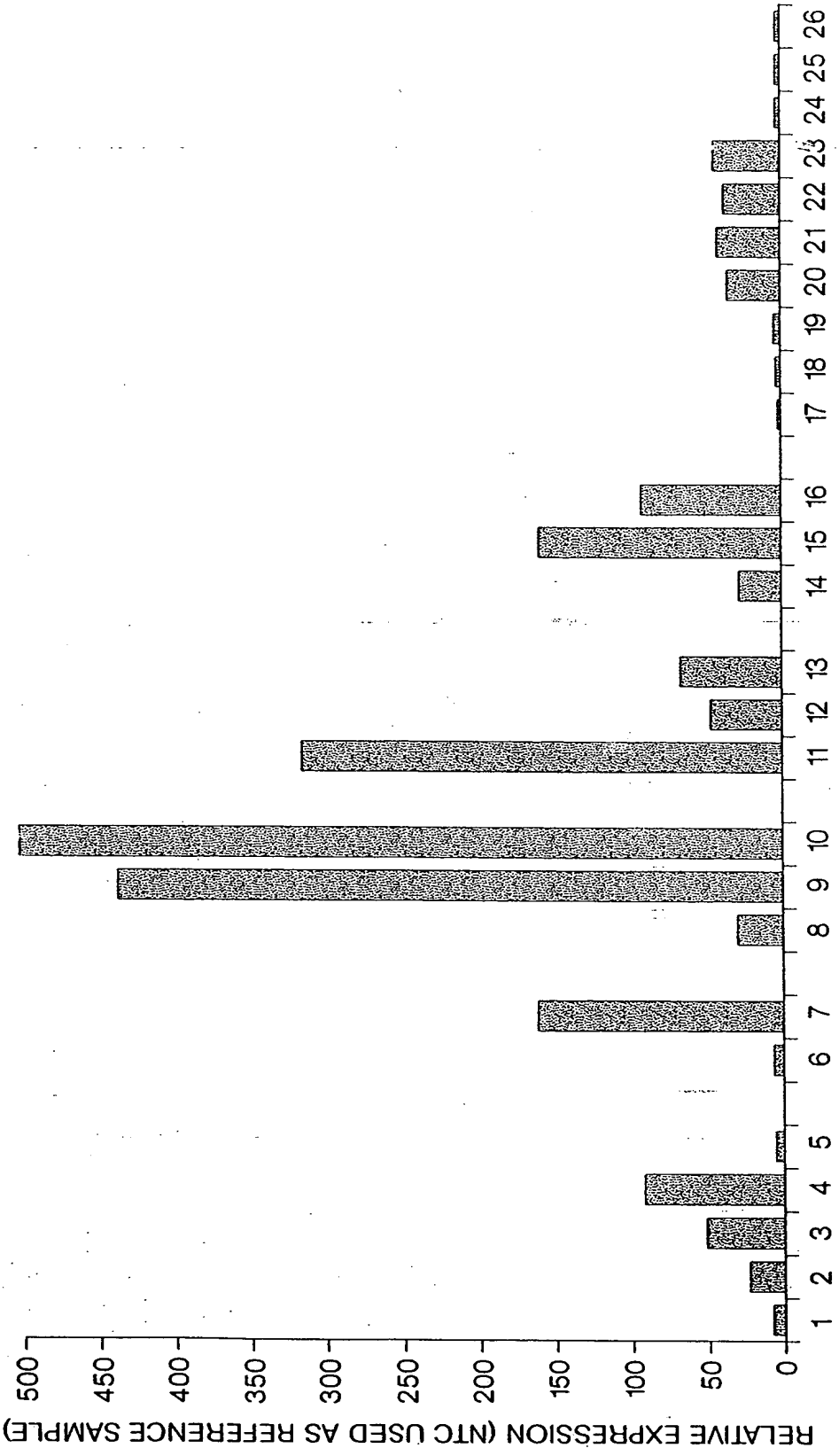

Fig. 28

Fig. 29

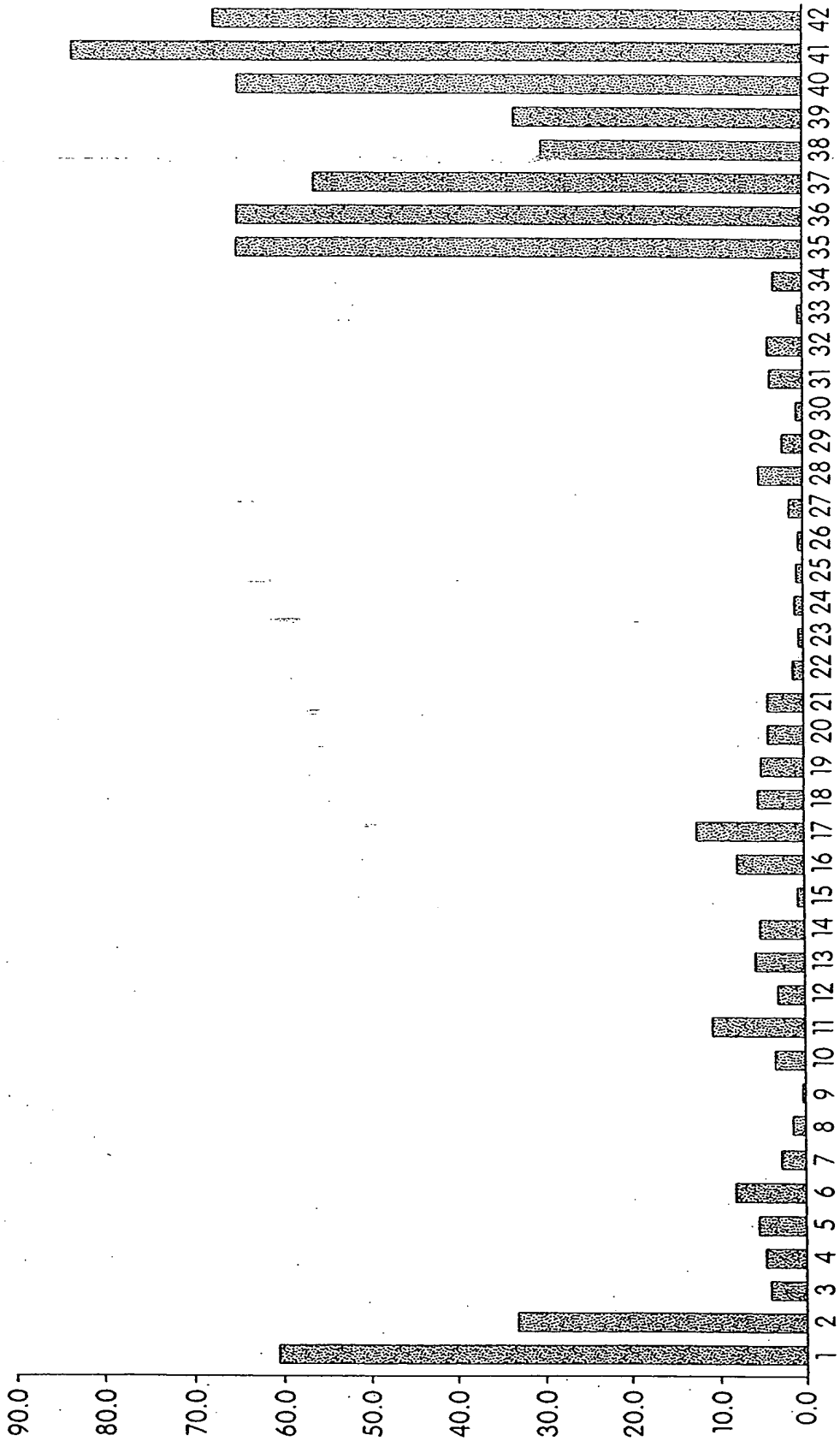

Fig. 30

GGAATGGATGCTGTTGGCTTAAACCTCCCCCTGCCCTGGGGGTTGCAACCAGGGTCTCTG

CAAAGCCAATCCTTTGTCATCCCGCTGTCCTGCAGAGCAAGATGGGGCTCATGGCTGTCC

TGATGCTACCCCTGCTGCTGCTGGGAATCAGCGGCCTCCTCTTCATTTACCAGGAGGCAT

CCAGGCTGTGGTCGAAGTCTGCCGTGCAGAACAAAGTGGTGGTCATCACAGATGCCATCT

CAGGACTGGGAAAGGAGTGTGCTCGGGTGTTCCATGCAGGTGGGGCAAGGCTGGTGCTGT

GTGGAAAGAACTGGGAGGGACTGGAGAGCCTCTATGCCACCTTGACCAGTGTGGCTGACC

CCAGCAAGACATTCACCCCCAAGCTGGTCCTCCTGGATCTCTCAGACATTAGCTGTGTTC

AAGATGTGGCCAAAGAGGTCCTGGACTGCTACGGCTGTGTGGACATCCTCATCAACAATG

CCAGCGTGAAAGTGAAGGGGCCTGCCCACAAGATTTCCCTGGAGCTTGACAAAAAGATCA

TGGATGCCAACTACTTCGGACCCATCACTTTAACCAAAGTTCTGCTTCCCAACATGATCT

CCAGGAGAACAGGCCAGATTGTGTTAGTGAACAACATCCAAGCGAAGTTTGGAATCCCGT

TCCGCACAGCTTATGCAGCCTCTAAGCATGCCGTCATGGGCTTCTTTGACTGCCTCCGAG

CCGAGGTTGAGGAATACGATGTTGTGGTCAGCACCGTGAGCCCAACTTTCATCCGCTCCT

ACCGTGCTTCCCCTGAGCAAAGAAACTGGGAGACATCCATTTGTAAATTCTTCTGCAGGA

AGCTAGCCTATGGCGTGCACCCGGTGGAGGTGGCTGAGGAAGTGATGCGCACAGTACGGA

GGAAGAAGCAAGAGGTGTTCATGGCCAACCCGGTTCCTAAGGCTGCCGTGTTCATCCGCA

CCTTCTTCCCTGAGTTCTTCTTCGCTGTGGTGGCCTGTGGGGTGAAGGAGAAGCTCAATG

TCCCAGAAGAGGGTTAACCTCGTGGCCAAAGGGGTCACTCAAGGGGAATAAAGGCTTTCC

TAGAGAAAAAAAAAAAAAAAAAAAAA

Fig. 31A

MGLMAVLMLPLLLLGISGLLFIYQEASRLWSKSAVQNKVVVITDAISGLGKECARVFHAG

GARLVLCGKNWEGLESLYATLTSVADPSKTFTPKLVLLDLSDISCVQDVAKEVLDCYGCV

DILINNASVKVKGPAHKISLELDKKIMDANYFGPITLTKVLLPNMISRRTGQIVLVNNIQ

AKFGIPFRTAYAASKHAVMGFFDCLRAEVEEYDVVVSTVSPTFIRSYRASPEQRNWETSI

CKFFCRKLAYGVHPVEVAEEVMRTVRRKKQEVFMANPVPKAAVFIRTFFPEFFFAVVACG

VKEKLNVPEEG.

Fig. 31B

```
GAP of: FrGcgManager_31_UFAHDJyG_  check: 516  from: 1  to: 936

M21481 ORF - Import - vector trimmed

to: FrGcgManager_31_VFA0zr_19  check: 2871  from: 1  to: 933

h21481 ORF - Import - vector trimmed

Symbol comparison table: /ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/
nwsgapdna.cmp
CompCheck: 8760

       Gap Weight:     12     Average Match: 10.000
    Length Weight:      4  Average Mismatch:  0.000

          Quality:   8220              Length:    936
            Ratio:  8.810               Gaps:      0
Percent Similarity: 88.103  Percent Identity: 88.103

      Match display thresholds for the alignment(s):
                 | = IDENTITY
                 : =   5
                 . =   1

FrGcgManager_31_UFAHDJyG_ x FrGcgManager_31_VFA0zr_19    ..

                .         .         .         .         .
  1 ATGGGGCTCATGGCTGTCCTGATGCTACCCCTGCTGCTGCTGGGAATCAG 50
    |||||  |||||||  | ||||||| ||||||||||||||||||||||||
  1 atgggagtcatggccatgctgatgctccccctgctgctgctgggaatcag 50

                .         .         .         .         .
 51 CGGCCTCCTCTTCATTTACCAGGAGGCATCCAGGCTGTGGTCGAAGTCTG 100
    |||||||||||||||||||||| ||||  |||||||||||||| |||||| |
 51 cggcctcctcttcatttaccaagaggtgtccaggctgtggtcaaagtcag 100

                .         .         .         .         .
101 CCGTGCAGAACAAAGTGGTGGTCATCACAGATGCCATCTCAGGACTGGGA 150
    | |||||||||||||||||||| ||||| ||||||||||||||||||||
101 ctgtgcagaacaaagtggtggtgatcaccgatgccatctcaggactgggc 150

                .         .         .         .         .
151 AAGGAGTGTGCTCGGGTGTTCCATGCAGGTGGGGCAAGGCTGGTGCTGTG 200
    ||||||||||||||||||||||||  ||||||||||||||||||||||||
151 aaggagtgtgctcgggtgttccacacaggtggggcaaggctggtgctgtg 200

                .         .         .         .         .
201 TGGAAAGAACTGGGAGGGACTGGAGAGCCTCTATGCCACCTTGACCAGTG 250
    |||||||||||||||| | || |||| ||| ||||   |||||| ||| |
201 tggaaagaactgggagaggctagagaacctatatgatgccttgatcagcg 250

                .         .         .         .         .
251 TGGCTGACCCCAGCAAGACATTCACCCCCAAGCTGGTCCTCCTGGATCTC 300
    |||||||||||||||||||||||||||| ||||||||||  |||| |||
251 tggctgaccccagcaagacattcaccccaaagctggtcctgttggacctc 300
```

Fig. 32A

```
301 TCAGACATTAGCTGTGTTCAAGATGTGGCCAAAGAGGTCCTGGACTGCTA 350
    |||||||| |||||||| | |||||||||| ||||| ||||||||| |||||
301 tcagacatcagctgtgtcccagatgtggcaaaagaagtcctggattgcta 350

351 CGGCTGTGTGGACATCCTCATCAACAATGCCAGCGTGAAAGTGAAGGGGC 400
    |||||||||||||||||||||||||||||||||| ||||| ||||||||||
351 tggctgtgtggacatcctcatcaacaatgccagtgtgaaggtgaaggggc 400

401 CTGCCCACAAGATTTCCCTGGAGCTTGACAAAAAGATCATGGATGCCAAC 450
    ||||||| |||||||| |||||||| ||||||||||||||||||||||||
401 ctgcccataagatttctctggagctcgacaaaaagatcatggatgccaat 450

451 TACTTCGGACCCATCACTTTAACCAAAGTTCTGCTTCCCAACATGATCTC 500
    ||||| || |||||||| || || |||| ||||||||||||||||||||
451 tactttggccccatcacattgacgaaagccctgcttcccaacatgatctc 500

501 CAGGAGAACAGGCCAGATTGTGTTAGTGAACAACATCCAAGCGAAGTTTG 550
    | |||||||||||||| || |||||||||||| || ||||||| ||||||||
501 ccggagaacaggccaaatcgtgttagtgaataatatccaagggaagtttg 550

551 GAATCCCGTTCCGCACAGCTTATGCAGCCTCTAAGCATGCCGTCATGGGC 600
    |||||||||||||| ||  |||| || ||||| ||||| || | | ||||||
551 gaatcccgttccgtacgacttacgctgcctccaagcacgcagccctgggc 600

601 TTCTTTGACTGCCTCCGAGCCGAGGTTGACGAATACGATGTTGTGGTCAG 650
    |||||||||||||||||||||||| || ||||||||||||||||  ||||
601 ttctttgactgcctccgagccgaagtggaggaatacgatgttgtcatcag 650

651 CACCGTGAGCCCAACTTTCATCCGCTCCTACCGTGCTTCCCCTGAGCAAA 700
    |||||||||||| |||||||||||| || |||| | | || ||||||
651 caccgtgagcccgactttcatccggtcgtaccacgtgtatccagagcaag 700

701 GAAACTGGGAGACATCCATTTGTAAATTCTTCTGCAGGAAGCTAGCCTAT 750
    |||||||||| | |||||||| |||||||| | ||||||||| ||||
701 gaaactgggaagcttccatttggaaattctttttcaggaagctgacctac 750

751 GGCGTGCACCCGGTGGAGGTGGCTGAGGAAGTGATGCGCACAGTACGGAG 800
    |||||||||||| || |||||||| |||||| |||||||||||| || ||||||
751 ggcgtgcacccagtagaggtggcggaggaggtgatgcgcaccgtgcggag 800

801 GAAGAAGCAAGAGGTGTTCATGGCCAACCCGGTTCCTAAGGCTGCCGTGT 850
    |||||||||||||||||| |||||||||||  | || ||||| |||||||
801 gaagaagcaagaggtgtttatggccaaccccatccccaaggccgccgtgt 850

851 TCATCCGCACCTTCTTCCCTGAGTTCTTCTTCGCTGTGGTGGCCTGTGGG 900
     | |||||||||||||||| |||||||| ||||| ||||||||||||||||
851 acgtccgcaccttcttcccggagttctttttcgccgtggtggcctgtggg 900

901 GTGAAGGAGAAGCTCAATGTCCCAGAAGAGGGTTAA 936
    |||||||||||||||||||||||| || ||||||
901 gtgaaggagaagctcaatgtcccggaggagggg... 933
```

Fig. 32B

```
GAP of: FrGcgManager_32_ZFA004eiD  check: 657  from: 1  to: 311

m21481 aa - Import - complete

to: FrGcgManager_32_AGAjaPna_  check: 9949  from: 1  to: 311

h21481 aa - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102
 Matrix made by matblas from blosum62.iij

        Gap Weight:      12      Average Match:  2.778
     Length Weight:       4   Average Mismatch: -2.248

           Quality:    1467             Length:     311
             Ratio:   4.717               Gaps:       0
Percent Similarity:  92.926   Percent Identity:  91.318

       Match display thresholds for the alignment(s):
                   | = IDENTITY
                   : =    2
                   . =    1

FrGcgManager_32_ZFA004eiD x FrGcgManager_32_AGAjaPna_ ..

      1 MGLMAVLMLPLLLLGISGLLFIYQEASRLWSKSAVQNKVVVITDAISGLG 50
        ||.||.||||||||||||||||||| ||||||||||||||||||||||||
      1 MGVMAMLMLPLLLLGISGLLFIYQEVSRLWSKSAVQNKVVVITDAISGLG 50

     51 KECARVFHAGGARLVLCGKNWEGLESLYATLTSVADPSKTFTPKLVLLDL 100
        |||||||| |||||||||||||| ||.||  | ||||||||||||||||||
     51 KECARVFHTGGARLVLCGKNWERLENLYDALISVADPSKTFTPKLVLLDL 100

    101 SDISCVQDVAKEVLDCYGCVDILINNASVKVKGPAHKISLELDKKIMDAN 150
        |||||| ||||||||||||||||||||||||||||||||||||||||||||
    101 SDISCVPDVAKEVLDCYGCVDILINNASVKVKGPAHKISLELDKKIMDAN 150

    151 YFGPITLTKVLLPNMISRRTGQIVLVNNIQAKFGIPFRTAYAASKHAVMG 200
        ||||||||| |||||||||||||||||||| |||||||| ||||||| :|
    151 YFGPITLTKALLPNMISRRTGQIVLVNNIQGKFGIPFRTTYAASKHAALG 200

    201 FFDCLRAEVEEYDVVVSTVSPTFIRSYRASPEQRNWETSICKFFCRKLAY 250
        |||||||||||||||:|||||||||||   ||| ||| || ||| ||| |
    201 FFDCLRAEVEEYDVVISTVSPTFIRSYHVYPEQGNWEASIWKFFFRKLTY 250

    251 GVHPVEVAEEVMRTVRRKKQEVFMANPVPKAAVFIRTFFPEFFFAVVACG 300
        |||||||||||||||||||||||||||:||||::|||||||||||||||||
    251 GVHPVEVAEEVMRTVRRKKQEVFMANPIPKAAVYVRTFFPEFFFAVVACG 300

    301 VKEKLNVPEEG 311
        ||||||||||| |
    301 VKEKLNVPEEG 311
```

Fig. 33